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esult Query
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                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: gb_ba:*
2: gb_ht:*
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ALIGNMENTS

JOURNAL MEDLINE REFERENCE AUTHORS	AUTHORS	REFERENCE	KEYWORDS SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 AF041051 LOCUS DEFINITION
Proc. Natl. Acad. Sci. U.S.A. 95 (9), 5407-5412 (1998) 98226828 2 (bases 1 to 1172) 4u.WJ. and Chiang, V.L.	Hu.W.J., Kawaoka,A., Tsal,C.J., Lung,J., Osakabe,K., Ebinuma,H. and Chiang,V.L. Compartmentalized expression of two structurally and functionally distinct 4-commarate:CoA ligase genes in aspen (Populus trompul)ides)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus. 1 (bases 1 to 1172)	quaking aspen. Populus tremuloides	promoter region. AF041051 AF041051.1 GI:3258638	AF041051 1172 bp DNA linear PLN 26-JUN-1998 Populus tremuloides clone Pt4CLlp 4-coumarate:CoA ligase gene,

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Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
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Lu,H., Zeng,Q. and Jiang,X.
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                                                    ATAAATTAGTGCATAAAATATAATGGATTGGTGGTCTGTGAAAAG-CAAGTGGAGGACAA
                                                             AAACTAAAATTAAAAAAGATTTAGATTATTAAATTATTAGGTTAATTCACGGGTTGGCTA
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                       GCCACCTCTCAAGTCAAAAGGCCACTTTCACAACCCAACCCAAATGGGAACCCACCACC
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ALLIAHPEISDAAVVGLKDEDAGEVPVAFVVKSEKSQATEDEIKGYISKQVIFYKRIK
RVFFIEAIPKAPSGKILKRKIKKEKLAGI"
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On Apr 2, 1999 this sequence version replaced gi:4337172.
* NOTE: This is a 'working draft' sequence It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACUUDDU4 104992 bp DNA linear Plasmodium falciparum chromosome 12, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-AUG-1998) Stanford Center, Stanford University, 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyman,R.W., Fung,E.L., Qin,F., Tamaki,T., and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; 1 (bases 1 to 104992)
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                                                           Similarity 45.:
02; Conservative
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/db_xref="taxon:5833"
/chromosome="12"
a 9326 c 9564 q 414
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, 45.3%;
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58842: gap of unknown length
91011: contig of 32169 bp in
91211: gap of unknown length
104992: contig of 13781 bp in
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                                                         Score 83; DB 2;
Pred. No. 6.8e-05;
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Avenue, Palo Alto,
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On Aug
* NOTE
* cons
                                                                                                                                                                                                                                                                                                                                                         AC004157 169546 bp Plasmodium falciparum chromosome PROGRESS ***, 2 unordered pieces.
                                                                                                             Direct Submission
Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                    HTG;
                                                                                                                                                            2 (bases 1 to 169546)
Hyman, R.W., Qin, F., Fung, E.L.,
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Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
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1 (bases 1 to 169546)
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                                                                                                                                                                                            Unpublished
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                         Aug 12, 2000 this sequence version replaced gi:8810447 NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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AL133402 9 Human DNA sequence from

93368 bp DNA 1: clone RP5-1077H22 on

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85631 ATACTTT
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                                                                                                                                                                        613
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                       793
                                                                                                                                              tcaattacatcacaaaaaacctaatcaaattaatatcttatgtgatataatttagaaata
                                                                                                                                                                                                                                                                                                              accactcgacttggggcattggtgatttttcaaatcacaactcaatttgaaaactaaaatt 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctctgtaattttgtgaaatagattaaaacagctcaatgtgaggtgaccagttgtcaaatg 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATAATAATATTATTATTATAATAATATATTAAATTAAATTAAATTTAATTAATTAA
                                                                                                                                                                                                                                                                                                                                                  aaaaaagatttagattattaaattattaggttaattcacgggttggctaatcaattatta
                                                                                                                                                                                                                                                                                                                                                                                                   ATATATTTAATTAAATTAAATTTATTTAATTAATTTAAATTAAATAAATAATAATTAAATT
                    atggatt
                                                            tttgtgtatctttggcagtaggtgagaggtgctgacaaataaaattagtgcataaaatata
                                                                                                           ttctaataaagcacttcctaattgttaaaatatatgtctaaaacactaataataaaattta 732
                                                                                                                                                                                                                                                  TTAAATAAATAATTAAAATAATAATAAATTAAATTAATTAATTAATAAATAAACATTA
                                             TTAAACAAATAATATAAATATTATATAATATTATTAATTAAATTAAATAATAATAATTATT
                                                                                                                                                                                                 TTTTTAATAATAATTTCTTAATTTATTTATTACATTATATATATATATATTTTTATTT
                                                                                                                                                                                                                       taaatgattaacctttaaatctcgagtttctcttataaaaaacacgtataattgggctag
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Similarity 45.3%;
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85625
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/db_xref="taxon:5833"
/chromosome="12"
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15381 c 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23466: contig of 23466 bp in length
23666: gap of unknown length
169546: contig of 145880 bp in lengt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            it is available and the accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15705 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 83; DB 2;
Pred. No. 6.1e-05;
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VERSION
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
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AL133402
AL133402.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP5-1077H22 is from the library RPGI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on May 23, 2000 this sequence version replaced gi:7939106. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requests: clonerequest@sanger.ac.uk
on May 23, 2000 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     feature key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      putative novel gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is the entire insert of clone RP5-1077H22
                                                                         6940. 7827
/note="11PBa repeat: m
7856. 9561
/note="11PB2 repeat: m
9565. 9598
                                                                                                                                                                                               /note="L
6632...6
                                                                                                                                                                                                                                      /note="L
4721..6
                                       /note="match: GSS: Em:AQ984702"
9599. .9750
                                                                                                                                                                                                                                                                               4299
                                                                                                                                                                                                                                                                                                                                                                                                                                         638
                                                                                                                                                                                                                                                                                                                    /note="AluSq repeat: matches 1.
complement(3971, .4298)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RPCI-5"
231. .537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/chromosome="6"
/clone="RP5-1077H22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Eutheria; Primates;
                                                                                                                                                                        5632. .6939
/note="Alux repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Alux repeat: matches 1. .301 of consensus"
                                                                                                                                                                                                                                                                                                 note="match: GSS: Em:AQ720689"
                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSx repeat: matches 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism≂"Homo sapiens"
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                                                                                                                                                                                                                                        -"L1PBa repeat: matches -1546.
.6631
  "4 copies 38
.9739
                                                                                                                                                                                                                   LlPBa repeat: matches -134.
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                                                                                                                                       matches 2762.
                      71% conserved"
                                                                                                                                                                            .310
                                                                                                                                                                                                                                                                                                                                                                             . 235
                                                                                                                                                                                                                                                                                                                                        . 304
                                                                                                                                                                                                                                                                                                                                                                                                                .303 of consensus"
                                                                                                                                                                                                                   .2762 of consensus"
                                                                                                                                     .3638 of consensus"
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                                                                                                consensus"
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complement(9796. .9835)
/note="match: GSS: Em:AZ002912"
9796. .9835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12016. .12384
/note="MLT1B repeat: matches 1.
13221. .13307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9842. 10202
/note="LLPB2 repeat: matches 5782. .6154 of consensus"
10724. .11003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9806. .9841
/note="match: GSS: Em:AG026544"
9807. .9841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: 9797. .9841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match:
9797. .9824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ745266" 9796. .9824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: 9796. .9823
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complement(9764. .
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                                                                            join(21618. .21754,
/gene="dJ1077H22.1"
24053. .24358
                                                                                                                                                                                                                                                        complement (19549
                                                                                                                                                                                                                                                                                                                                  /note="L1M4c repeat: matches 15208. .15761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(9796.
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join(<21618...21754,25301...>25
                                                                                                                                                                                                                                                                                                 /note="MER66B repeat: matches 1.
17062. .17326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluJo repeat: matches 1.
11341. .11501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: GSS:
                                                                                                                 /product="dJ1077H22.1 (putative novel protein)"
join(21618. 21754,25301. .25566)
                                                                                                                                                      /note="match: ESTs: Em:AA960797"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: STS:
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  /note="MIR repeat: matches 43.
26551. .26628
                                                           note="MER33
                                                                                                                                                                                                 /gene="dJ1077H22.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MER5B repeat: matches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note-"match: GSS: Em:AZ028723"
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                                    "MER33 repeat: matches 7. .323 of consensus" .25647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9824
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .13693
                                                                                                                                                                                                                                                                                                                                                                                                                  VL1 repeat: matches 595. .1036 of consensus"
.4463
                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 550.
                                                                                                                                                                                                                                                                           repeat: matches 28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .9823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Em: AQ014122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mer ta 73% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Em: AQ014122"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Em: AQ598220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Em: AQ324044 Em: AQ373503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Em: 252156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Em: AQ745266"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Em: AQ745589"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Em: AG019010 Em: AG026881"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Em: G34561"
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                    .246 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 289
                                                                                                                                                                                                                                                                                                                  . 486
                                                                                                                                                                                                                                                                               . 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .638 of consensus"
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Query Match
Best Local Similarity
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                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                      /note="23 copies 4 mer
46483..46558
/note="38 copies 2 mer
47326..47676
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/note="12 repeat: matches 2677. .2710 of consensus"

34405. 34634

/note="LIMB8 repeat: matches 5857. .6120 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38000. .38111
/note="28 copies 4 mer tata 67% conserved"
38001. .38112
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27163. .27450
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="5 copies 38
46228. .46383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46186.
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41413. .41819
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                                                                                                                                                                                                                                                                                                                                                                                                  /note="3 copies 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="14 copies 4 mer agaa 73% conserved"
46186. .46375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 21. .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ430150
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43137. .43480
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42349. .42490
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41820. .41874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MER33 repeat: matches 22. .294 of consensus"
37654. .37931
note="LLMC5 repeat: matches 7507. .7777 of consens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L2 repeat: matches 2411.
37369. .37635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MER74A repeat: matches 132. .528 of consensus"
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                                                                                                                                                                                                                                                       Score 82.2; DB 9;
Pred. No. 9.5e-05;
0; Mismatches 298;
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                                                                                                                                                                                                                                                                                      Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 20, 2001 this sequence version replaced gi:15148276. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boushayki, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
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Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                             Center code: WIBR
                                                                                                                                                                                   Center: Whitehead
                                                                                                                                                                                                                         -- Genome Center
                              Project
name: L5662
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SEQUENCING
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DNA

linear

VRL

complete

genome

Oma, E.,

Kutish, G.F.

and

Rock, D.L.

Island

Research

Animal Disease arch Service, P.O.

entomopoxvirus"

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Kutish, G.F.

and

Rock, D.L.

Poxviridae;

Entomopoxvirinae;

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nes 224; Conserv
                                                                                                                    aattaataattattttttctaataaagcacttcctaattgttaaaatatatgtctaa 713
                                                                                                                                                                                                                                                      ttattggatttgaatgaactcaattacatcacaaaaaacctaatcaaaattaatatcttat 533
                                                                                                                                                                                                                                                                                                                                                          gttggctaatcaattattaattaaatagagatagtatttttgataatttaattaaaatt 473
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                                                                               acactaataataaaatttattt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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1 15157; contig of 155157 bp in 155158 155257; gap of 100 bp 155258 185699; contig of 30442 bp in 1 Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP11-709B3"
/clone_lib="RPCI-11 Human Male
42163 c 43800 g 50039 t
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Pred. No. 0.00012;
0; Mismatches 338
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-MAY-1998) Microbiology, Plum Is Center, U.S. Dept. Agriculture, Agricultural Box 848, Greenport, NY 11944-0848, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Melanoplus sanguinipes
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Melanoplus sanguinipes
AF063866
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onso,C.L., Tulman,E.R., Lu,Z.,
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                                                                                                                                                                                                                                                                                          /translation="MAEKRNVKVKLVEPDVNKSLSTIIEALQNEIQKSIQDQSNILKQ NLSEDIMNEVEKFESQVTELTNMLKNYVISTIEEKIDNYVNSLIS" complement (6347. .6814) /gene="MSV004"
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SDKFTYNLINVVIISNNKILQINNIDKKYEKVFNRYLIFNYDHVILTQQIDEI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6051./gene="MSV002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MFLYLISQNINNVSKISISNTQSMFLYLISQNINNVSKISISNT
QSMFLYLISQNINNVSKI"
                                                                                                                                                                                                                                                            complement(6347.
/gene="MSV004"
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/gene="MSV002"
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/isolate="Tucson"
                                            protein"
                                                                                                                                                                                                                        protein"
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                                                                                                                                                                                                                                    /product="ORF MSV004 155
                                                                                                                                                                                                                                                /codon_start=1
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complement(12364. .../gene="MSV010" complement(12364. ../gene="MSV010" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="ORF MSV008 leucine rich repeat gene family protein, similar to Amsacta moorei entomopoxvirus Q3 SW:P28854"
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8831. .9058
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KECELITFQNQFEICEICYKNKVFMYCSHCTDITEVDELNGKCKNCNFINKSYYAYIG
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                                                                                                                                                                                                                                                                                  /product="ORF MSV009 leucine rich repeat gene family protein, similar to Amsacta moorei entomopoxvirus Q3 SW:P28854"
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IKLNCGYYITDFKFLEBLINLQKLNISSNSYSNISKCKLPISLIKFKSSYCDITNFK
FLEBRLINLETLFIYMNSKSNISICKLDFSLIKHNETEFVDIKNIKFIERLINLESLASS
SRSSRNISQCILPTSLIVLDLYSCHIKNFKFLEBLINLKKLNISDNGDSNISKCKLBI
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NCNECKIIDFKFLESLINLEILDISYNKNSNIYKCKLSSLLKNLNCNECKIIDFKFLE
SLINLEILDVSYNKNSNIYECTLPISLIELKCISCKIIDFKFLESLINLEILDVSSNE
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                                                                                                                                                                                                                                                                                                                                                                                                                           complement(11374. .12138)
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10282. .10476
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                                                                                                                  aggtgaccagttgtcaaatgaccactcgacttggggcatggtgatttttcaaatcacaac
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NNIISNISNYKLSKTIKKFICARCAITDFTFLEELINLEILDVSYNHKLNISECELPI
SLKKLYCNNCFIKNNTLLKKLINLTILNISFNKITDFKFLENLTNLEILDISENKNSN
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ICVRCDIKDFWFLEKLFRLØMLDISYNYIKSNISKCKLPISLIELYCKNCTNUNFYFL
NDLPRLEILDISCNNKIININNIRLSKKLIKLNCSNNUNSDIKFLEHLSKLEILNISV
NKISYIYNYKLPNNLLELNCKYNNIKWFKFIERLHNLKKLNISNNKKSNISKCKLPQT
IINLAIKACDITDESFLEPLANLEKLNITEENYDNETMLSKCKLPVSLRVLKSTDFNV
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CSDCYKTKDFKFLERLINLQKLNISYTFSSNISTCELTSTLVELNCSTCKINNFTFIE
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KKLNISDNRNLKITECKLPISLIELDCSSCDITDFKFLEPLINLKKLNISDSRNLKII
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14293. .15810
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/gene="MSV013"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aaattaattattattttttctaataaagcacttcctaattgttaaaatatatgtcta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgtgatataatttagaaatataaatgattaacctttaaatctcgagtttctctttataaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATATCTAATATTTGTAAATTATTAAAAATTTCTTAAAAAATTTAAAAGATTTAATATTACAT 227799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATATTTAATTTAATTAATGATTCTGGTAATTCGTAGCACCATATGTATTATTATTAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTCCTGTAAATTATTTAAATTTTTGAGGTATCTATCATTTTCAATATAACATTTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                            CB10 1SA, UK
On Dec 16, 19
For more info
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG
                                                                                                                                                                                                                                                                                                phage etc
                                                                                                                                                                                                                                                                                                                correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector.
                                                                                                                                                                                                                                                                                                                                                                                        see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: sequence is unfinished and does not necessarily represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-SEP-1998) P.falciparum Genome Sequencing The Sanger Centre, Wellcome Trust Genome Campus, Hinxto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bowman,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malaria parasite P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL031746.9 GI:6594243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFMAL1P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 67970)
                                                                                                                                                                                                                                                                                                                                                                                                                           Dec 16, 1999 this sequence version replaced gi:5763807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barrell, B.
   overlap)"
                                                    aa, similarity: UPF0006 family YBL055C/YBL0512/YBL0511, YBF5_1
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                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                                                                                                                                                                                     'db_xref="taxon:5833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Churcher, C., Harris, B.,
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                                  316,
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                                BLO511, YBF5_YEAST (418 aa), fasta
E(): 1.1e-12, (33.2% identity in 271
                                                                                                                                                                                                                                        falciparum'
                                                                                                                                                                2598, 2748. . 2848, 2990.
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                                                                                       protein, len:
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                                                                                                                                                                .3276))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cambridge
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                                                  NHLQNDAFYNTYKKFSQTEIDEISRDFLSIGKNASSSSGIKNNIKNIIDNIKFYEN
DYIINEISTKKMEKOSLNENRSLPNVNIYN MYSOVESYTFYTYSCINLFNVFVKIF
MSFYVFHIKIGSNSVGIAIMLSILALYSAMILFEELSSLFKSKYLLTRDKRIDNMHIVL
KEFKLIKMFNNESFAFKYINLFRMKEBKYCKIRLYLSNIGUFISSISDIVEVUIFFI
YLKDRLNKKEEIKFTSIIMPLYVYKILLSNVANFPNLVNNVMEGIVNIKRLNNYINDH
LYYNDIKNYFMYRTRYNBDYNIVVDKTFLQNENITSHDOGTSHNLKHLKNVIKNKLIN
MFKYFEFYHKNNYKRNIINQLLSGLLKNVDDMTNKKICFGEHSNSTYNYNSSHIHE
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TDYFRKKLFDEVELNYKHSNKMIYKEAPFVKGNTESVSFEIDSINKEYIKKMKKNY
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YTLDTTTSHYLHYKHSKRKIYKNY
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TILQKQVRYLEYFVILPIISLVTSGICFSMIIYGNITSAIKVHNNILYSILNAPLYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YISFLKDFKVFSGLVVVMIMFFHLFFEALLHFYFHLFTINLKVSLMYFLYKINLCSNN
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/db_xref="GI:6594246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14884. .20352
/gene="MAL1P3.03"
14884. .20352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein, MAL1P3.02"
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/db_xref="G1:6594245"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contains possible signal sequence"
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complement(2984..2989)
/gene="MAL1P3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="potential splice complement(2849..2861) /gene="MALLP3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MAL1P3.01"
/note=""""
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSLKSLENINAVKKIPLNLLLLETDAPWCGVKKTHASYEYIKDTYEKRAYTNLKKIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEKDKEYLENLKNKIIKYPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLVQMFN
LPMFLHMRNCSETFFKIVDIYKFLFEKNGGVIHSFTDKEDIVHIIVQNYKNLYIGVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNNVDKIIITCTCLAEIDKSLKICETYDPEGKFLYLSAGVHPTNCYEFIDKNKHEEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="conserved hypothetical protein, UPF0006 family"
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/db_xref="GI:6594244"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="possible cen1,
14884. .20352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MAL1P3.02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MAL1P3.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MAL1P3.0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MAL1P3.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .5496
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/gene="MALIP3.04"
/note="potential splice acceptor sequence"
complement(32669. .32674)
/gene="MALIP3.04"
/note="potential splice donor sequence, aaa/9
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                  /gene="garp"
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/note="potential splice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36744...36749

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/note="potential splice donor sequence,

36854...36863
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TKIWKETIKKMRQNYEKETDNMNHNWRDFMWHYKWANIYLYKVHKLINITLKDLTNPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                len: 203 aa, similarity: P. falciparum chromosome 2, PFB0110W, 096126 predicted integral membrane protein (255 aa), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity in 191 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(31966. .32476,32675. .32775))
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/note="MAL1P3.04, conserved hypothetical membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subunit rRNA genes 23896. .31533
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/note-"region containing small subunit,
/note-"region small subunit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEEFAKISNKENASMNKENEL
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KITVEGADIRTYNRKGEDSIIOILAGSSFVFYNMNIRTFIDFYNNFTDDEIVHALKLN
GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINOSNDNTILLTNDCIRYLSLVRLYLN
KTEKKKKQEEKEKKKQEKERKKQEKKERKQKEKEMKKQKKTEKERKKKEEKEKKKKK
                                                                                                                                                                                                                                                                  /gene="garp"
/note="MALIP3.06, garp, len: 673 aa, similarity
identical to GARP_PLAFF (678 aa), fasta scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="hypothetical protein, MAL1P3.05"
/protein_id="cAB63560.1"
/db_xref="GI:6594248"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDKEETITTWIKWIQEDIEYFLFNLQVEWLRILTLELFYKNKE" complement(32477. .32486)
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/db_xref="GI:6594247"
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                                                                                                                                                                                                                                                  identity in 678 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MAL1P3.05"
/note="MAL1P3.05,
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                                                                                                                                                                                                                             /codon_start=
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RESULT 9 AL513330/c

DEFINITION LOCUS

AL513330 202645 bp Homo sapiens chromosome 1 clone I PROGRESS ***, 7 unordered pieces.

RP11-469E8,

linear , *** SE

SEQUENCING

HTG 10-JUL-2001

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tcttataaaaaacacgtataattgggctagatttaacagctattattcaaactggccagg 642
                                                                                                                                                                                                                                                                                                    aatgaataatatgattgattattctctgtaattttgtgaaatagattaaaacagctcaat 289
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                                                                                                                                                                                                                         taatatcttatgtgatataatttagaaatataaatgattaacctttaaatctcgagtttc
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/note="potential splice acceptor sequence"
^^mnlement(40204. .40209)
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EHKEEEHKKEEHKSKEHKSKGKKDKGKKDKGKHKKAKKEVKKHIVVKNYIEDE
DKDGVEIINLEDKEACEEQHITVESRPLSQPQCKLIDEPEQLILMDKSKVEEKNLSIQ
EQLICTIGRVNVVPRDNHKKKMAKIDEAELOKQKHVDKEEDKKEESKEVEEESSKEVQ
EDEEEVEEDEEEEEEEEEEEEEEEEEEEEDEVEEDDAEEDDDAEEDDDAEED
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/note="potential splice donor sequence, aag/gtaaca"
join(45401._46396,46562._50233)
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Pred. No. 0.00022;
0; Mismatches 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator ET-amersham; 0% of reads Chemistry: Dye-terminator Big Dye; 99% of reads
Consensus quality: 200455 bases at least Q40
Consensus quality: 201365 bases at least Q20
Consensus quality: 201775 bases at least Q20
Insert size: 202045; sum-of-contigs
Insert size: 161399; 19.6% error; agarose-fp
Ouality coverage: 6.15x in Q20 bases; sum-of-contigs Quality
coverage: 7.70x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On May 7, 2001 this sequence version replaced gi:13396737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Sanger Centre
Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: bA469E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved.
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  (bases 1 to 202645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7984 8083: gap of 100 bp
8084 16795: contig of 7983 bp in length
16796 16895: gap of 100 bp
16896 73805: contig of 8712 bp in length
73906 13905: gap of 100 bp
73906 147587: contig of 77777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTGS_PHASE1; HTGS_CANCELLED
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                                           fragment_
16896. .7
                                                                                                                                    vector_side:left"
/note="assembly_fragment:01698
fragment_chain:1"
                                                                                                                                                               clone_end:SP6
                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                 /note="assembly_fragment:01844
fragment_chain:1"
                                                                                                                                                                                                                                                      /clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                              /clone="RP11-469E8"
                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                   note="assembly_fragment:00874
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202645: contig of 21026 bp in length
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                                                                                                                                                                                                                                                                                                                                     235;
Waterston, R.H.
                                                 Waterston, R.H.
                                                                                                                                          AC096550 AC013666
AC096550.1 GI:15638715
                                                                                                                                                                                AC096550 181486 bp
Homo sapiens chromosome 2 clone
                                    The sequence of Homo sapiens clone
                                                            Mammalia; Eutheria; Pr
l (bases 1 to 181486)
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                     Unpublished
                                                                                                      Homo sapiens
                                                                                                                             HTG; HTGS_PHASE1;
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Submitted (18-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Sep 18, 2001 this sequence version replaced gi:7382143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big Dye; 100% of reasonably program: Phrap; version 0.990319
Consensus quality: 176334 bases at least Q40
Consensus quality: 178430 bases at least Q30
Consensus quality: 178430 bases at least Q20
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Contact: submissions@watson.wustl.edu
------ Project Information
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   Direct Submission Submitted (02-NOV-1998) The Institute for Genomic Research, Submitted (02-NOV-1998) The Institute for Genomic Research, Medical Center Drive, Rockville, MD 20814, USA
                                                                                        Erratum:[[published erratum 4;282(5395):1827]]
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Science 282 (5391), 1126-1132 (1998)
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/protein_id="AAC71888.1"
/db_xref-"GI:3845199"
/translation="MFALKKNTVREGFVNICFSYLKKLYLKSNFVTVNLNYETNNEKR
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11241. .14606
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Davy-Carroll, L. Dederich, D.A. Delaney, K. R. Delgado, O. Denn, A.L., Ding, Y. Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Huly, S., Huber, J., Jackson, L. Jackson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Krarlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, L., Li, J., Li, J., Li, M., Karlson, R., Lucier, A., Lucier, R., Luna, R., Martinez, E., Masson, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K., Morgan, A., Mayyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojubokan, I., Rolfe, M., Stone, H., Sutcon, A., Svatek, A., Tabor, P., Tannerisa, K., Tang, H., Stone, H., Sutcon, A., Svatek, A., Tabor, P., Thomas, N., Tannerisa, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Warfen, R., Washindron, C., Vinson, R., Washindron, C., Warten, R., Washindron, C., Vinson, R., Washindron, C., Warten, R., Washindron, C., Warten, R., Washindron, C., Warten, R., Washindron, C., Washindron, C., Warten, R., Washindron, C., Washindro
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                       Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D. Weinstock,G. and Gibbs,R.
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Direct Submission
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JOURNAL REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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130944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 19031 bases at least Q40
Consensus quality: 191911 bases at least Q30
Consensus quality: 192818 bases at least Q20
Estimated insert size: 190344; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 17.7x in Q20 bases; sum-of-contigs est:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: HBYI Center clone name: RP11-707P20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; L08821
                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="Xp"
/clone="RP11-707P20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 130843: contig of 130843 bp in length
130943: gap of unknown length
4 189214: contig of 58271 bp in length.
Location/Qualifiers
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Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Elwards, C.C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M.,
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Earnhart, C., Edgar, D., Escotto, M.,
Earnhart, C., Edgar, D., Escotto, M.,
Earnhart, C., Edgar, D., Escotto, M.,
Earnhart, C., Edgar, M., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Hartin, Haward, M., Garner, T., Garza, N., Gill, R.,
Earnhart, C., Hartin, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Holloway, C., Hollins, B.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Ledi, B., Lewis, L.C.,
Kratovic, J., Kureshi, A., Lucier, R., Luna, R., Ma, J.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G.,
Neurie, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
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                         aacctaatcaaattaatatcttatgtgatataatttagaaatataaatgattaaccttta
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Homo sapiens chromosome Xp clone RP11-539J11, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
AC108683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.R., Davila,R., Da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Bennon,J., Bimage,K., Blankenburg,K., Bonnin,D.,
                                                      Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                        atggtgatttttcaaatcacaactcaatttgaaaactaaaattaaaaaagatttagatta 389
attttgataatttaattaaaattttattggatttgaatgaactcaattacatcacaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see http://www.hgsc.bcm.tmc_edu/docs/Genbank_draft_da
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64557
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196473
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Chemistry: Dye-terminator Big Dye: 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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3 171642: gap of unknown length
3 196472: contig of 24830 bp in length
3 196572: gap of unknown length
9 208319: contig of 11747 bp in length.
Location/Qualifiers
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/clone="RP11-539J11"
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                                                                                                                                                                                                                                                                                                                                            Score 78.4; DB 2;
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                                                                                                                                                                                                                                                                                                                                    On May 14, 2001 this sequence version replaced g1:2982535 g1:2982536 g1:2894454 g1:2982554 g1:2982562 g1:2894489 g1 g1:2982574 g1:4493931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T., Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Feltwell,T., Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holrod,S., Hornsby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S., McLean,J., Moule,S., Mungall,K., Murphy,L., Oliver,K., Quail,M.A., Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S., Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
                                                                                                                                                                                                                                                                                             see
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Eukaryota; Alveolata; Apicomplexa;
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                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                more information about this sequence or the Malaria Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., Skelton,J.,
join(322. .603,826. .1023,1197. .1301,1458. .2942)
/gene="pFC0575w, MAL3P5.1"
/gene="pFC0575w, MAL3P5.1"
/gene="pFC0575w, MAL3P5.1"
/note="pFC0575w, MAL3P5.1"
/note="pFC0575w, (MAL3P5.1), Hypothetical protein, len:
/note="pFC0575w (MAL3P5.1), Hypothetical grotein, len:
                                                                                                                                                                                                    /organism="Plasmodium falciparum'
/strain="3D7"
                                                                                                                                                                                /db_xref="taxon:5833"
                                                                                                                                  /clone="MAL3P5"
                                                                                                                                                      /chromosome="3"
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RSPQ1YRKRFKRSRIKNVSFKKKGKFLFLFEBLLKKGFSFLGFWRNQYDQKYIDDVIS
NINNLTRIKQVTHKKKSNEFTKENIKQILLHCVFSKIDFKIINNLSVIIKHGPGHOMSNIT
VHSILNQISEKVKERKDAENYLALHLFLLHCVFSKIDFKIINNLSVIIKHGPGHOMSNIT
VHSILNQISEKVKERKDAENYLALHLFLLHCVFSKIDFKIINNLSVIIKHCHFFLCYNLLER
IKBECVGDLIRKIITYNLFICTLIYFTYCMCLLIKYISHLCIFFFFFFCYNLLER
IYBECVGDLIRKIIFSNYDNINNDISIDKDMYMNNPIDVNINNISLDEKIKEGFERD
DDENLKELKDTYEQFQLFNDNIIKYIEEDQPLYNINDNSNINDNNNINTMKNKHKIK
DTYNDLDDVDYEKEBDLVIQKNIDDYIYKNTIGMNKSLEFKNQFIEGADIEFQNFLS
NVNLDQHGRVKSNDENTKSTEHIKNKNTIINKGYDFELIQNOMENNFIKNUTUNISND
ISNNENIIKKLKLNQSDEDINITSDLIYERLFRYVLWYIQKIEYLKFKYQYDIINEQ
YPIIKNEKTVLDLLNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDKNNQMENQKNSKNY
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/gene="PFC0580c, MAL3P5.2"
complement (3354...6644)
/gene="PFC0580c, MAL3P5.2"
/note="PFC0580c, MAL3P5.2), Hypothetical protein, 1
1097 aa, possible signal sequence, predicted using hexexon"
                                                                                                                                                                                                                                                                                                                                                                                                         DNICRICLNINTNITINFYMINILKYICYKNMEIILLNYNHIEDMKKKINGKNNINTS
LFRYYISFFFKKEENHIYDLFEDGMMHLHKENDKFYNYSKENTHNNIYKYISDNY
LFRYYISFFFKKEENHIYDLFEDGMMHLHKENDKFYNYSKENTHNNIYKYISDNY
KYJSHNISSSURCSFKNLKKQOTDDNYTHIIMCKEKYPMNKSDHEKKNNINTCGNINIEK
KYDKHINSSSURCSFKNLKKQOTDDNYTHIIMCKEKYPMNKSDHEKKNNITCGNINILKE
COKKDILKKIYFLKGNKLLKQOTDNYTHHIMCKEKYPMNKSDHEKKNIHILEKKME
FDKDNKIYLKKBADYMNLKRBILKRFSKNEERENINSFASFFLLSKNIIFFEDEIG
RSRDNTIYLNAVDKETNKTTTNNNNDNNDNICSNNDHJCSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNDYNTHKKEKRKRI
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complement/??:
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/protein_id="CAB38969.2"
/db_xref="GI:7711065"
                                          /gene="PFC0581w", 7829,7912...7940,8064...8106, join(7669...7117,7800....7829,7912...7940,8064...8106, 8302...8368.8568...8641,8713...8812,8924...9006,9122.9369...9505,9613...9838)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIKKIRIHNKCSYIPLLFLNIYDSYIYKNKILRWLPKFRKRRKDKEBYYYITOMVRK
KRREAJKYNEISDEQNLFNKEYIYEIYUSYSUKYGILSPHLSLYILKNISEHCVNIYP
SLYYYNKLDNKKHULINEKKLKYFKQLINDEHYQQAPTNHTHHNUNUNNKKLSEHCINIHSC
KNTNISSYSTYNNMEKENINIYDKYNIHNFYTEKSISYKDENCOHITLNMIYLLNOTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Hypothetical protein, PFC0580c"
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8302. .8368,8568. .8641,8713. .8812,8924. .9006,9122.
9369. .9505,9613. .9838)
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/note="predicted splice acceptor sequence for (revised of PFC0575w)"
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/note="predicted splice donor sequence
PFC0575w (revised)"
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LYTQRIQNCCDIFSYIYKKYNFNEKNPFLNYLYYELHYIVYSEKKKKKKFFSFISSSP
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IDIVKFKDLYYCMINNINNIFSYIHKVDHNECVYRIFKAYNKILLYEYNYLNEKENIY
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/note="PFC0581w, hypothetical protein, len: 324 aa, revised: new gene prediction, splicing prediction very
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prC0581w"
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/translation="mkkkkkhyssikfvnvdknkyvlcskdyiriinymiglhiferll /kranslation="mkkkkkhyssikfvnvkkdjidglekdwfnifpylisesikodndfs ndikttyfahdkolassffeshknkkpdtvnsfomaospeyiftnikfeshtwssfak lkykdeelvskknnfsfsalsndsnsvtkkyivdltlldniiesetkynfasvgkvvv TLKKEKKKIWNRLLLSKEKYPNMQVWWDMKEKRIHIITFVTINLFFLLSLSHRYHDSV /codon_start=1 /product="hypothetical protein, PFC0581w" /protein_id="cAB90285.1" /db_xref="GI:7711066" acceptor sequence for exon 2 of

QNFLKEEKNNSDKLQDDIDEDEEKYFDEEILREAKKKSEEYDKDDEEL"

/note="potential splice acceptor sequence ${\tt PFC0581w"}$ donor sequence donor sequence for for for exon exon exon N 4 w of

acceptor sequence donor sequence for for exon exon 4 of. of.

splice acceptor sequence donor sequence for for exon exon G of ហ of.

acceptor sequence for exon δ of

donor sequence sequence for for exon exon δ of. 7 of.

acceptor donor sequence sequence for for exon exon 8 of 7 of.

/gene="PFC0581w" /note="potential splice donor sequence for exon acceptor sequence for donor sequence for exon exon 9 9 æ of. of. of

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AUTHORS
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Matches 265; Conserv
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Submitted (30-JAN-2002) DOE Joint Genome Institute, 2800 Mi
Drive, Walnut Creek, CA 94598, USA
On Jan 30, 2002 this sequence version replaced gi:15290376.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 5 clone ACO26698
                                                                                               Direct Submission
Submitted (23-MAR-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
3 (bases 1 to 192731)
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Mammalia; Eutheria; Primates;
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DOE Joint Genome Institute and
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Pred. No. 0.00047;
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Search completed: Job time: 6859 sea July 30, 2002, 11:28:25

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Page 18

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AAS61076	ABL32325	ABL32058	AAI61373	ABL18982	AAS46506	ABL34073	ABL32462	AAX58644	ID
Human gene regulat	Human immune syste	Human immune syste	Soybean 318013 reg	Drosophila melanog	Tumour suppressor	Human immune syste	Human immune syste	Aspen 4-coumarate	Description

ALIGNMENTS

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RESULT
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        12-NOV-1998;
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                                                                                                                                                        Populus tremuloides
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 Human immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 435;
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system associated gene SEQ ID NO:
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Pred. No. 0.00037;
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genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
         The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-digomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g.
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                                                                                                                                                       Claim
                                                                                                                                                                                      analysing
                                                                                                                                                                                                                   Fragments of chemically modified genes associated with tumour suppressor
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and
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11-JUL-2000;
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                                               soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhgl or an Rhg4 SCN resistant allele. The nucleic acids can be used for investigating rhgl or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins. The present sequence is a nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified nucleic acid for producing a soybean plant having soybean cyst nematode resistance and for use in plant breeding programs - \,
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
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                                                       2001WO-EP07537
  2000DE-1032529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                     rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%;
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                                                                                                                                                                                                                                                                                                               arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                       arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiasthmatic;
                                                                                                                                                                                                                                                                                                               bowel disease;
                                                                                                                                                                                                                                                                                                                                                                       anaemia;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloi leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytosine
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for diagnosi:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention provides a number of human immune system associated es which are modified by the methylation of cytosines. The sequences
TAATTCCAACAATAATATATTTTTTA
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                      cactaataataaaatttatttgtgta 740
                                                                      attaataattattatttttctaataaagcacttcctaattgttaaaatatatgtctaaa 714
                                                                                                               CATTACATATTATAACATATTACATATCATATTTCAATATCATTTCTAATTTAAAT
                                                                                                                                                                                                                                          tattggatttgaatgaactcaattacatcacaaaaaacctaatcaaaattaatatcttatg 534
                                                                                                                                                                                                                                                                                                  aatttgaaaactaaaattaaaaaagatttagattattaaattattaggttaattcacggg 414
                                                                                                                                                                                                                                                                                                                                                                                                                      gtgaccagttgtcaaatgaccactcgacttggggcatggtgatttttcaaatcacaactc
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTATACATTCTTTTAAAAATATTTAAAAATAACTTATTTCCACTATAATTCAATATA 5241
                                                                                                                                                                                                                            ATTATCGCTTTACCGCAAATATCTTTAATATAAAAAA --TAAACACTTCATAAATACAAA 5301
                                                                                                                                                                                                                                                                                   CTTAATAAAAAACATTTCTAACTTTAACTTTACAAATTAATCATAATTAACTTAAAATAA
                                                                                                                                                                                                                                                                                                                                         TCTTCTAAATCAAATCCTCTCATAAAACTTTCATCAAACTTAACTTTCTTATATTCACAA 5479
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                                                                                                                                                                                            tgatataatttagaaatataaatgattaacctttaaatctcgagtttctcttataaaaaa 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
240; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69.6; Di
Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
 5095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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Best Local
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic;
  646
                                                                                                                                           531
                                                                                                                                                                       468
                                                                                                                                                                                                   591
                                                                                                                                                                                                                             408
                                                                                                                                                                                                                                                                                 348 acaactcaatttgaaaactaaaattaaaaaagatttagattattaaattattaggttaat
                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                           tcacgggttggctaatcaattattaattaaatgatagtatttttgataatttaatt
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attattaaaattaattattattttttctaataaagcacttcctaattgttaaaatat
                                                                                                            tatcttatgtgatataatttagaaatataaatgattaacctttaaatctcgagtttctct
                                                                                                                                                                   aaaattttattggatttgaatgaactcaattacatc--acaaaaaacctaatcaaattaa
                                                                                                                                                                                                 tataaaaaacacgtataattgggctagatttaacagctattattcaaactggccaggaca
                                                                                   AACTTTATCTCTTATAAATAAAATAAAAAAAAAACAAAAATTTAAATTTAATTATATAA
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                                                                                                                                                                                                                                                                                                                                                                                     6071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                                                                Conservative
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                   BP; 1973 A; 46 C;
                                                                                                                                                                                                                                                                                                                             5.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin
                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                           Score 69; DB 24;
Pred. No. 0.0013;
0; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                   1013 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IJ
                                                                                                                                                                                                                                                                                                                                                                                   3039 T; 0 other;
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                                                                                                                                                                                                                                                                                                                265;
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                                                                                                                                                                                                                                                                                                                                       Length 6071;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system associated
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RESULT 9
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                                                                                    The invention relates to 224 nucleic acid sequences comprising at 1% 18 bases of a chemically pretreated gene associated with gene regulated selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The plants of cytosine methylations of the plants of cytosine methylations.
The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such generality are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiadisorders, haemophilia, solid tumours and cancer, werner syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiac damage; inflammatory response; Haemophilia; Werner syncasthma; HDR syndrome; congenital heart defect; Saethre-Chotzen renal disease; Preeclampsia; cardiac allograft vascular disease
                                                                                                                                                                                                                                                            New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS61076
                                                                                                                                                                                                                 Claim 1;
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01-SEP-2000;
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07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene regulation-associated gene oligonucleotide #31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                 OHS
                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                          regulation, and therapy
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                 cardiac
                                                                                                                                                                   regulation
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RESULT 10
AAK82710/c
ID AAK827
XX AAK827
XX AAK827
XX O7-NOV
DT 07-NOV
XX
DE Human
XX Human;
KW Cytost
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OS Homo s
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PN W02001
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PF 17-JAN
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       17-JAN-2001; 2001WO-US01354
                                       09-AUG-2001
                                                                                                                                         cytostatic;
                                                                                                                                                                                                                              07-NOV-2001
                                                                                                                                                                                                                                                                                                AAK82710 standard;
                                                                       WO200157182-A2
                                                                                                                                                            Human;
                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37522.
                                                                                                                                                                                                                                                                AAK82710;
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                                                                                                                                                       immune; haematopoietic; immune/haematopoietic antigen;
                                                                                                                                         gene
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                                                                                                                                       therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                DNA;
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Pred. No. 0.00:
0; Mismatches
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11-JUL-2000

126-JUL-2000

26-JUL-2000

11-AUG-2000

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04 - FEB - 2000

24 - FEB - 2000

02 - MAR - 2000

16 - MAR - 2000

17 - MAR - 2000

17 - MAY - 2000

07 - JUN - 2000

28 - JUN - 2000

07 - JUL - 2000

07 - JUL - 2000

07 - JUL - 2000
2000US - 0190076
2000US - 0198123
2000US - 0198123
2000US - 0210467
2000US - 0215135
2000US - 02151880
2000US - 02151880
2000US - 0217496
2000US - 0217496
2000US - 0225513
2000US - 0225513
2000US - 0225513
2000US - 0225513
2000US - 0225757
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2000US - 0225
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2000US-0180628.
2000US-0184664.
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02-0CT-2000
02-0CT-2000
03-0CT-2000
13-0CT-2000
20-0CT-2000
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01-DEC-2000
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Nucleic acids encoding useful for preventing,
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02-OCT-2000;
                                         2001-483426/52
                                                                                             HUMAN
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2000US-0246523.
2000US-0246525.
2000US-0246526.
2000US-0246528.
2000US-0246528.
2000US-0246609.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0249210.
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2000US-0249213.
2000US-0249213.
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2000US-0241826.

2000US-0244617.

2000US-0246474.

2000US-0246475.

2000US-0246476.
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2000US-0241221.
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2000US-0249217

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2000US-0250160.
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2000US-0237037
                                                                                             GENOME
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3-0251989.
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3-0251479.
                                                                                             SCI INC
human immune/hematopoietic antigen diagnosing and/or treating cancers
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             polypeptides,
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) collynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastases of haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represent sequences used in the exemplification of the
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                                                           aattaatatcttatgtgatataatttagaaatataaatgattaacctttaaatctcgagt
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48.2%;
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Pred.
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RESULT 11
ABL33451/c
ID ABL334
XX
AC ABL334
XX
DT 26-MAR
DT 26-MAR
XX
KW Human;
KW Human;
KW antiar
KW neurop
KW antiir
                          Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
  antiinflammatory;
                 antirheumatic; antiarthritic;
                                                                                                                                                                    ABL33451
                                                                                    Human
                                                                                                              26-MAR-2002
                                                                                                                                       ABL33451;
                                                                                  immune
                                                                                                                                                                    standard;
                                                                                                             (first
                                                                                  system
  cancer; eye
                                                                                                                                                                    DNA;
                                                                                    associated
                                                                                                             entry)
                                                                                                                                                                  19787
  disease;
                 antidiabetic;
                                                                                 gene
                                                                                    SEQ
 arteriosclerosis; anaemia;
                                                                                    ID
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TATATAAATATATAATAGTATATTATATATATATAT

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                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                   2194
                                                                                                                                                                                                                                                               2430
                                                                                                                                                                                                                                                                                                                  2490
                                                                                                                                                                                                            2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acute myeloid leukaemia; Alzheimer's disease; AIDS; neurofibromatosis; rheumatoid arthritis; psoriasis;
2134 TATTACCCATACTAAAATACAATAATCTTAA
                                                                                                      2251
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19787 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-)
                         696
                                                                                                                                576
                                                                                                                                                                                                                                                                                        396
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rear acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal osine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention provides a number of human immune system associated
                     gttaaaatatatgtctaaacactaataataa 726
                                                  CTATTTTCATATATACACTTAAAAATAACCTA--
                                                                                                                    attttcaaatcacaactcaatttgaaaactaaaattaaaaaagatttagattattaaat
                                                                           ggccaggacaattattaaattaattattattttttctaataaagcacttcctaatt
                                                                                                                                                       CCAAAATAACGATATTTCGTAATTAAAAATTAAAAAACTCATTA-TAACTATTTTTCCTC
                                                                                                                                                                                 atcaaattaatatcttatgtgatataatttagaaatataaatgattaacctttaaatctc
                                                                                                                                                                                                           gataatttaattaaaattttattggatttgaatgaactcaattacatcacaaaaaaccta
                                                                                                                                                                                                                                                              TCTAATTATAATTTAACATTTCAACTAAAAATAACTTAAAAATTCAATAAAACTATTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1424; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000DE-1032529
.2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                  6302 A; 270 C;
                                                                                                                                                                                                                                                                                                                                                                                5.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin
                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                Score 68.6; DB : Pred. No. 0.0016
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   3756 G; 9459 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
                                                                                                                                                                                                                                                                                                                                                                    184;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                           Length 19787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epilepsy;
bowel disease;
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RESULT

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ABL34175/c
ID ABL341
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 48.8
Conservative
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24968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatlc; antiarthritic; antidiabetlc; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; ana acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 including eye diseases such as retinopathy, neovascular glaucoma a macular degeneration, arteriosclerosis, annemia, cancer, acute mye leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL34175 standard; DNA; 113515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 113515 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL34175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                            210
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                                                  390
                                                                                                                                                                                                                                                                       270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis and treatment of diseases associated with osine methylation
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                                                                                                                                                                                                                                                                                                                         AAAAAATAAAAATATATATCAAAACTAACTATTTAATAACATATATAAACCTTTTAA 25089
ATATTACTTTATAAACAATAATCCAAATATAAAAAATTAAAAATTAACACAAACAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2148; 32pp + Sequence Listing; German.
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system disease; cytosine methylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35172 A; 1174 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%;
48.8%;
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Pred.
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No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22520 G; 54649 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24;
).0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                       194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 113515;
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RESULT 1
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                                           Query Match
Best Local S
Matches 224
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                                                                                                                                      The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADIS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcarative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; a acute myeloid leukaemla; Alzheimer's disease; Albs; epiley neurofibromatosis; rheumatoid arthritis; psoriasis; bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
01-SEP-2000;
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                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-130909/17.
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                 87
                                           Local Similarity
mes 224; Conserv
                                                                                                                                                                                                                                                                                               diagnosis and trosine methylation
tttatatatatatatatgcatgcatgaggaccatggctatgatgaaggttaatagagg 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aacctaatcaaattaatatcttatgtgatataatttagaaatataaatgattaaccttta
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                                                                                                                 10191
                                                                                                                                                                                                                                                                   SEQ ID NO 2228; 32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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2000DE-1043826.
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                                                                                                                BP;
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                                                                                                                2964 A;
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                                                        5.8%;
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                                                                                                                                                                                                                                                                                                                                                                                  Berlin
                                                                                                                285 C;
                                             0;
                                          Score 67.4; DB 24; Pred. No. 0.0026; 0; Mismatches 261;
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                                                                                                              2323 G;
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                                                                                                                T; 2
                                           Indels
                                                                   Length
                                                                                                                other;
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RESULT 14
ABL32487/c
ID ABL324
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AC ABL324
XX
AC ABL324
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                                                                                                                                                                                                                                        30-JUN-2000;
01-SEP-2000;
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Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with

gene, useful abnormal

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RESULT 1
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Best Local Similarity
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  31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzhéimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                       17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                             WO200157182-A2
                                                                                                                                                                                                       Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41082
                                                                                                                                                                                                                                    07-NOV-2001
                                                                                                                                                                                                                                                                                        AAK86270 standard; DNA; 9706
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                                                                                                                                      Homo sapiens
                                                                                                                                                                cytostatic;
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47.7%;
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                                                                                                                                                                 vaccine;
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Pred. No. 0.
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ine; metastasis; ds.
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Nucleic acids encoding useful for preventing,
metastasis
    preventing,
          human immune/hematopoietic diagnosing and/or treating
              : antigen
                         polypeptides,
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2001-483426/52.

Barash

SC,

SM:

Search completed: July 30, Job time: 4595 sec

2002, 11:22:21

Disclosure; SEQ Ħ NO 41082; 3071pp + Sequence Listing; English

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CNS0155H	CNSU14PQ	CNSOOKHX	CNS00LT2	CNS004ZW	CNS00DKY	CNS00FUH	AI909641	CNS00FYG	CNS02T50	CNS00A3W	CNS015WU	CNS009G1	CNS02ON7	CNS016YR	CNS00EQL	CNS010MP	CNS07JUX	BH177277	CNS00BO1	CNS020K7	CNS0161D	CNS00DKY	CNS001FB	AL565457	AL565457	CNS00EQL .
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                                                                                                                                                  AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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AL063971
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                 fly), ger
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- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
- The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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7ative 101; Mismatches 247;
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                                      TTTWTTTWTATWTTTATATWTWWAAAAWAWWAAWTWTATTTTTWTTATWATTWATA
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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    Web : www.genoscope.cns.fr)

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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29P01 of RPCI-98 library from Drosophila melanogaster (frui
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/db_xref="taxon:727"
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Location/Qualifiers
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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segref@genoscope.cns.fr
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                                      TTAAAATTTWAATWTTTATTTWTTTWTANNTTTWTATATNTATTWWATWWWWAWAAAAWA
                                                                   gtgaggtgaccagttgtcaaatgaccactcgacttggggcatggtgatttttcaaatcac
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Human gene number estimate provided by genome wide analysis using
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                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
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                                                                                                                                              and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR05N11"
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Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila
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Drosophila melanogaster genome sur
BACR08K08 of RPCI-98 library from
                                                                                                                         isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 1101)
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                                                                  Mismatches 184;
melanogaster"
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survey sequence TET3 end of BAC #
rom Drosophila melanogaster (fruit
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RESULT 1
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                                                                                                                                                                                                                                Genoscope.

Direct Submission
Submitted (16-FEB-2000) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                         Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                          African malaria mosquito.
Anopheles gambiae
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Anopheles.
1 (bases 1 to 910)
                                                                                                                                                   Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and W Direct Submission
Submitted (16-FEB-2000) BBMI, Institut Pasteur,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic survey sequence.
AL142826
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(bases 1 to 910)
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/clone="BACR08K08"
/note="end : TET3"
a 120 c 103 g
/organism≈"Anopheles
/strain="PEST"
                                                Location/Qualifiers
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39.2%;
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                                                                                                                                                                                       and Weissenbach, J.
                                                                                                                                                                                                                                         National de Sequencage
segref@genoscope.cns.f
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Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                   CNS010MP

134 UP

Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04L20 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                   Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                     Drosophila melanogaster
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                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                            fruit fly.
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/clone="06E14"
/clone_lib="NotreDame1"
/note="end : SP6"
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                                                                                                                                     segref@genoscope.cns
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/clone="BACN04L20"
/note="end : T7"
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                        scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ
This sequence is a single read and was generated
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Roest-Crollius, H., J
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/db_xref="taxon:99883"
/clone="222L11"
/clone_1ib="G"
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/note="Genoscope sequence ID : COA
/note="Genoscope sequence ID : COA
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Pred. No. 0.00013;
4; Mismatches 160;
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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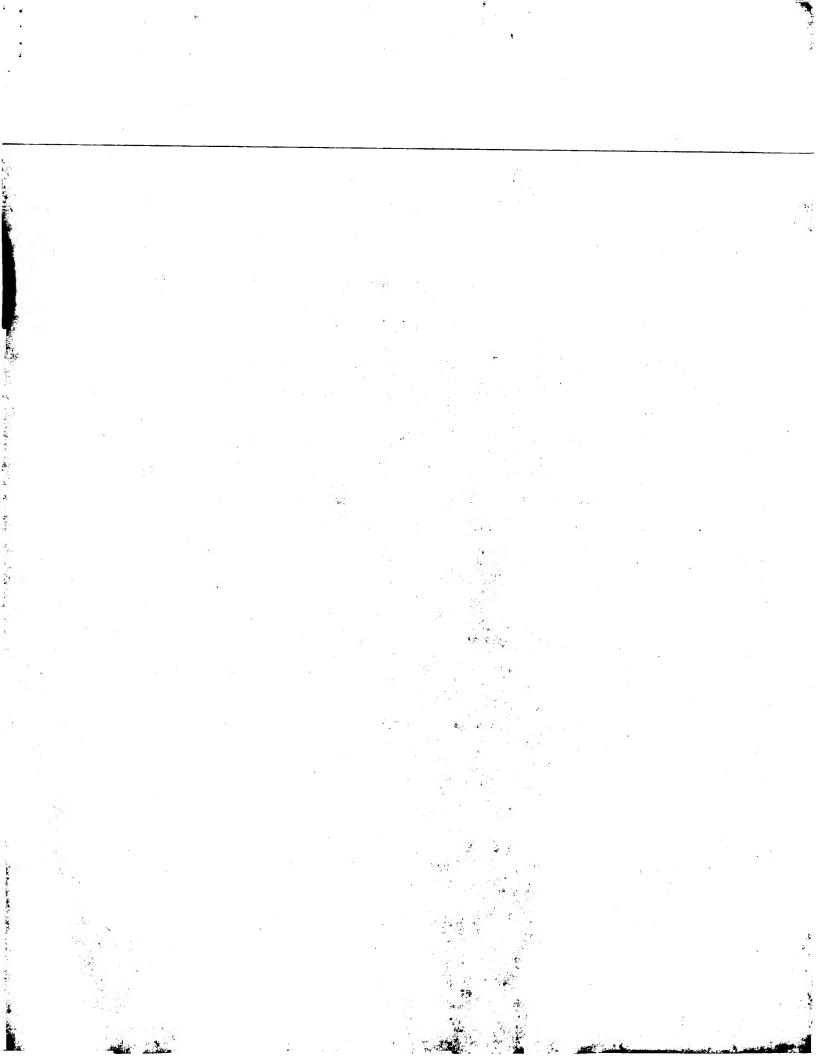
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This sequence is a single read and was generated as part of a lar
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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1 (bases Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Rouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot
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/clone_lib="G"
/note="Genoscope sequence ID : C0BG101CD11LP1-end :
/note="Genoscope sequence ID : C0BG101CD11LP1-end :
/note="Genoscope sequence ID : C0BG101CD11LP1-end :
/note="Genoscope sequence ID : C0BG101CD11LP1-end : ID : C0BG101CD
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Bernot,A. and
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                                                                   aaatcacaactcaatttgaaaactaaaattaaaaaagatttagattattaaattattagg 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttaattcacgggttggctaatcaattattattaattaaaacgatagtatttttgataatt 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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                                                                       CMCCAACCCACATMCMACMCCCMMMTTMAACCAAATMAMAAAACCMTMMAACTCAAMMCC
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Search completed: July 30, 2002, 10:38:02 Job time: 5471 sec



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                        GenCore version 4.5
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US-08-852-629-15
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US-08-998-416-288
US-09-316-083-2
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US-07-991-867B-32

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Sequence 1137, Ap

Sequence 36, Appl

Sequence 32, Appl

Sequence 8, Appl

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Sequence 11, Appl

Sequence 11, Appl

Sequence 15, Appl

Sequence 288, Appl

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Sequence 1036, Ap	Sequence 1036, Ap	Sequence 683, App	Sequence 5, Appli	Sequence 701, App	Sequence 3, Appli	Sequence 11, Appl	Sequence 595, App	Sequence 595, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 13, Appl	Sequence 534, App	Sequence 13, Appl	Sequence 5, Appli	Sequence 191, App

ALIGNMENTS

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PATENT NO. 6239264

GENERAL INFORMATION:
APPLICANT: Pohlippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Wendland, Jurgen
APPLICANT: Mendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/998,41
FILING DATE: 24 DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            TELEPHONE: 919-541-858
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
                     MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                            LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: No. 6239264artis Co
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
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PAG1692RP
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ER: PF/5-30306/A/CGC1976
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US-08-883-795A-36
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Best Local Similarity
Matches 208; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5985607
GENERAL INFORMATION:
                                                                  APPLICATION NUMBER: US/08/883,795A FILING DATE: 27-JUN-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Gravelle, Micheline NAME: Gravelle, Micheline
                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Recombinant DNA Molecules and Expression TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Delcuve, GenevappLICANT: Awang, Gregor
                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
                          TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                             ZIP: M5H 3Y2
                                        REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
                                                                                                                                                                                                                                                                                           STREET:
             TELEPHONE:
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            (416)
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361-1398
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48.3%;
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Pred. No. 3.5e-05;
0; Mismatches 217;
                                                                                                                                                             Version
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; IMMEDIATE SOURCE:
; CLONE: Rh 32
US-08-883-795A-36
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US-07-991-867B-32
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ORIGINAL SOURCE:
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36
                                                                     ZIP:
                                                                                COUNTRY:
                                                                                                STATE:
                                                                                                           CITY: Gainesville
                                                                                                                                      ADDRESSEE:
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                                                                                                                         E: David R. Saliwanchik
2421 N.W. 41st Street, Suite
                                                                                  USA
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Pred. No. 3.5e-05;
Prematches 232;
    Version
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US-08-107-755A-32
; Sequence 32, Application US/08107755A
; Patent No. 5721352
; GENERAL INFORMATION:
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Best Local Similarity
Matches 205; Conserv
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 0:
FILING DATE: 30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/6 FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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Moyer, Richard W.
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12-DEC-1992
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48.0%;
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Pred. No. 4.2e-05;
0; Mismatches 221;
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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TELEFAX: (904) 372-58 INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: U.S.
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APPLRAMT: Gruidl, Michael E.
TITLE OF INVENTION: NO. 5721352el
NUMBER OF SEQUENCES: 40
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LENGTH: 660 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 31,79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/827,658 FILING DATE: 30-JAN-1992
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                                                                               attttttctaataaagcacttcctaattgttaaaatatatgtctaaacactaataataaa 727
                                                                                                                                                          gctagatttaacagctattattcaaactggccaggacaattattaaaaattaataattatt 667
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                                                                                                                                      ATAATATCTAAAAATAAATTTGGTAACTTTAATAATGTTTTTCCTATTAGTATAGTTGAG
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2421 N.W. 41st Street, Suite
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Pred. No. 4.2e-05;
0; Mismatches 221;
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: Sequence 32, Application US/08544332

: Patent No. 5935777
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                                                                                     Query Match
Best Local
                                                                     Matches
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                                                                                                                                                                                                                                                           TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Hall, Richard L.
APPLICANT: Gruiddl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07 FILING DATE: 30-JAN-1992 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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ADDRESSEE: Gerard H. Bencen
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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91
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/657,584 FILING DATE: 19-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 01 FILING DATE: 19-AUG-1993
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                                                                     Local Similarity
es 205; Conserv
                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                TELEPHONE:
AATATTAATATTAAAAAAAATTAGTTAATTTAGAAGAATTGCATATAATATATTATGAT 150
                                                                                                                                                                                                          nucleic acid
DEDNESS: double
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                                                                                                                                                                                                                                           660 base pairs
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                                                                     Conservative
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                                                                     0;
                                                                 Score 61.4; DB 2;
Pred. No. 4.2e-05;
0; Mismatches 221;
                                                                                                  Length 660;
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US-07-991-867B-8
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            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Moyer, Richard W. APPLICANT: Hall, Richard L. APPLICANT: Gruidl, Michael E. APPLICANT: Gruidl, Michael E. TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression
                                       TELEPHONE: 904-375-8100
                                                                                    FILING DATE: 19-PEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                          APPLICATION NUMBER: US 0: FILING DATE: 30-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
SEQUENCE
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CTTY: Gainesville
                                                                    REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C3
                                                                                                                                APPLICATION NUMBER: US 07/657,584 FILING DATE: 19-FEB-1991
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CHARACTERISTICS:
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                             904-372-5800
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                                                                           APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
***CORRESPONDENCE ADDRESS:
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Local Similarity 48.0%;
nes 205; Conservative
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                               STATE:
                                           CITY:
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                                                                                                                                                                            INFORMATION:
32606
                                           Gainesville
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                            Florida
                                                      E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
              U.S.A.
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852..1511
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Best Local S
Matches 205
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REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                   1002
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LENGTH: 1511 base pairs
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
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OPERATING SYSTEM:
SOFTWARE: Patent!
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nes 205; Conserv
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                                                ATAATATCTAAAAATTAAATTTGGTAACTTTAATAATGTTTTTCCTATTAGTATAGTTGAG
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DEDNESS: double
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19-AUG-1993
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19-FEB-1991
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Pred. No. 5e-05;
0; Mismatches 221;
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US-08-544-332-8
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ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1362 AAAAAAT 1368
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ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
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FILING DATE: 12-FEB-
PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: WO 92/14818
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
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TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
                                                                                                                        FEATURE:
                                                                                                                                                                                                   EATURE:
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Best Local S
Matches 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6106825
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Li, Yi
APPLICANT: Hall, Ric
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1122
                                                                                                                                                                                                                        CURRENT APPLICATION DATA
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                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
     TELECOMMUNICATION INFORMATION: TELEPHONE: 407-426-7500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429
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                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "'
                                                NAME: Bencen, Gerard H REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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205; Conserv
                                                                                                                                                                                                                                                                                                                                                                             32606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Saliwanchik, Lloyd & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                               PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
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                                                                                                                                                                                                 US/08/852,629
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Pred. No. 5e-05;
0; Mismatches 221;
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787

INFORMATION FOR SEQ ID NO:

11:

TELEFAX:

407-839-8589

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RESULT 10
US-08-852-629-15
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                                                                                                                                                                                                                                                Sequence 15, Application US/08852629
Patent No. 6106825
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W
APPLICANT: Li, Yi
APPLICANT: Hall, Richard L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                   TITLE OF INVENTION: ENTOMOPOXVIRUS-VERTEBRATE GENE DELIVERY TITLE OF INVENTION: VECTOR AND METHOD NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4535
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LENGTH: 4810 base pairs
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                                                                                    STATE: Flor
COUNTRY: U.
ZIP: 32606
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                               STREET: 2421 N.W. CITY: Gainesville
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Local Similarity 48.0%;
les 205; Conservative
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                                                                                                                     Florida
                                                                                                                                                 E: Saliwanchik, Lloyd & Saliwanchik 2421 N.W. 41st Street, Suite A-1
                                                                                                    U.S.A.
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     Version
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                                                                                                                                       Sequence 288, Application US/08998416 Patent No. 6239264
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Best Local Similarity
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                                                                                                                           GENERAL
                                     APPLICANT:
APPLICANT:
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APPLICANT:
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              TITLE
                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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              S,
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                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
DEDNESS: both
              INVENTION:
Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                              Philippsen, Pete
Pohlmann, Rainer
Steiner, Sabine
                                       Wendland, Jurgen
Knechtle, Philipp
                                                                    Mohr, Christine
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Pred. No. 6.3e-05;
0; Mismatches 221;
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Best Local Similarity
Matches 310; Conserv
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MOLECULE TYPE:
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
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REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
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                                TATTAAAATATTATTAGATATTATTTTTCTTTAATAAATTATTAAAATAGATTATCAAT
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Pred. No. 4.9e-05;
0; Mismatches 378;
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; LENGTH: 1431
; TYPE: DNA
; OTGANISM: Saccharomyces co
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1428)
US-09-316-083-2
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APPLICANT: The Institute of Physical and Chemical APPLICANT: The Institute of Physical and Chemical TITLE OF INVENTION: Endonuclease FILE REFERENCE: PH-651
CURRENT APPLICATION NUMBER: US/09/316,083A
CURRENT FILING DATE: 1999-05-20
EARLIER APPLICATION NUMBER: J998/141861
EARLIER FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
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Best Local Similarity 51.68;
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665 GTAATTGTAATA
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                      ctaataataaaa
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                                                                                                                                              gtataattgggctagatttaacagctattattcaaactggcca-ggacaattattaaaat 656
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Pred. No. 0.0001;
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Best Local Similarity
Matches 207; Conserv
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
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MEDIUM TYPE: Floppy disk
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3059 AAAGATTTAATTTTTTCAATTTTAACAATACTTTTTGTAATATTATGTTTAAATTTAATT 3118
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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Rood, Julian
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3770..4013
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45.8%;
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Pred. No. 0.00013;
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RESULT 14
US-08-998-416-1137/c
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                                          Query Match
Best Local Similarity
Matches 224; Conserv
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                                                                                                                                                                                                                                                                        TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0
FILING DATE: 31-DEC-1996
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ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
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Steiner, Sabine
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Knechtle, Philipp
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/ENTION: GENOMIC DNA SEQUENCES
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IBM PC compatible
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                                          Score 58.8; DB 4;
Pred. No. 0.00016;
0; Mismatches 237;
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TELEPHONE:
TELEFAX: 91
INFORMATION FOR
SEQUENCE CHARAC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
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                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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ZIP: 27709
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 CHARACTERISTICS:
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PENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
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MOLECULE TYPE: DI
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ORGANISM: PAGI:
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Pred. No. 0.00016;
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JOURNAL MEDLINE REFERENCE ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT AF041051 LOCUS REFERENCE AUTHORS DEFINITION AUTHORS TITLE quaking aspen.

Populus tremuloides

Populus tremuloides

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 1172)

Teai.C.J., Lung,J., Osakabe,K., Ebinuma,H. an AF041051 1172 bp Populus tremuloides clone Pt4CLIp promoter region. AF041051 AF041051.1 GI:3258638 Proc. Natl. 98226828 Compartmentalized expression of two structurally and functionally distinct 4-coumarate:CoA ligase genes in aspen (Populus Hu, W.J., Ka Chiang, V.L. 2 (bases 1 to 1172) Hu,W.-J. and Chiang,V.L. tremuloides) Kawaoka, A., Tsai, C.J., Lung, J., Osakabe, K., Ebinuma, H. and Acad. Sci. U.S.A. 95 (9), 5407-5412 (1998) DNA linear PLN 26-JUN 4-coumarate:CoA ligase gene, PLN 26-JUN-1998

Result No.

Score

Query Match Length DB

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Description

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Submitted (01-JUL-2001) Biology, 1
Beijing Qinghua East Road No. 35,
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
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Lu,H., Zeng,Q. and Jiang,X.
Genomic DNA sequence of 4-coumarate:CoA ligase
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/db_xref="taxon:3693"
/clone="Pt4CL1p"
/tissue_type="leaf"
1. .>1172
AGPVLAMCLAFAKEPFDIKPGACGTVVRNAEMKIVDPETGASLPRNQPGEIÖIRGDQI
MKGYLNDPEATSRTIDKEGWLHTGDIGYIDDDDELFIVDRLKELIKYKGFQVAPAELE
ALLIAHPEISDAAVVGLKDEDAGEVPVAFVVKSEKSQATEDEIKQYISKQVIFYKRIK
                                                   AANPESTPAELAKHAKASRAKLLITQACYYEKYKDFARESDYKVMCVDSAPDGCLHFS
ELTQADENEAPQVDISPDDVVALMYSKGTGLFKGVMLTHKGLITSVAQQVDGONPNL
YEHSEDVILCVLPMEHIYALMSINLGCIRVQASILLHWRFEIGSELGILEKYKYKSIAP
VPPPVMMSIAKSPDLDKHDLSSLRMIKSGGAPLGKELEDTVRAKFPQARLGQGYGMTE
                                                                                                                            /translation="MNPQEEFIFRSKLPDIYIPKNLPLHSYVLENLSNHSSKPCLING
ANGDVYTYADVELTARRVASGLNKIGIQQGDVIMLFLPSSPEFVLAFLGASHRGAIIT
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/protein_id="AAL02144.1"
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Submitted (25-APR-2001)
University, 4444 Forest
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Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda; Chromadorea;
Rhabditoidea; Rhabditidae; Peloderinae; Cae
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Caenorhabditis elegans
AF067942
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Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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16; Conser
                                                                                                          Submitted (05-OCT-2001) Department of University, Genome Sequencing Center,
                                                                                                                                                                                           Submitted (07-SEP-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                 Submitted by:
                                                                                                                                                      Waterston, R.
                                                                                                                                                                University, Genome Sequencing Center, Louis, MO 63110, USA
8 (bases 1 to 40114)
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Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England email: rw@nematode.wustl.edu
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                                        Department of Genetics, Washington St. Louis , MO 63110, USA, and
                                                                 Genome Sequencing Center
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Caenorhabditis
 jes@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INV 05-OCT-2001
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                                                                                                            St.
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neighboring submissions
                          NOTICE: This sequence may not be the entire insert of this It may be shorter because we only sequence overlapping sectionee, or longer because we provide a small overlap between
                                                                          sections
                                                                                                            clone
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more than one m13 subclone. regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phith an alternate sol); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemist

NEIGHBORING COSMID INFORMATION

cosmid CELZK6 cosmid is Y39D8B; 3' cosmid is Y39D8A. Actual start of this is at base position 1 of CELZK6; actual end is at 40114 of . The orientation of this cosmid is unknown. .

the Coding ing sequences below are predicted
program Genefinder(P. Green and I
Location/Qualifiers ۲ from computer L. Hillier, ms in preparation). analysis, using

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ZK6.7"
join(5937..60
7589..7687)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ZK6.8"
join(2105. .2307,3036. .3223,3287. .
3956. .4127,4306. .4441,4490. .4708)
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/codon_start=1
/note-"similar to lysosomal acid lipases (SW:P38571); coded for by the following C. elegans cDNAs: yk263b10.3, yk263b10.5, yk3088.5, yk522a3.3, yk522a3.5, yk722d9.5, yk722d9.3, yk733a11.5, yk733g10.5, yk736f6.5, yk736f6.3, yk733g10.3, yk851d01.5"
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DAGFDVWLGNMRGNTYSMKHKDLKPSHSAFWDWSWDEMATYDLNAMINHYLEVTGQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSEESLPPSSGSKMSPRAFELLCVVMLGFGHLCIMTGCDSQAFI
LESVINSIHERDPARINSHAGYYGQATCYLAFVETCLVSPTFLYATSAKTTLIIAAAC
FTSFPLGELYTNQYYLFESAALMGVFFALYYGHGGYLTSHSTRKTIESVSISWAIG
SSCMIVGAGIIALITFLTAGQGSEVAMDLANATVTQHFERRESDTEIYLLESVFAAIG
FVGCITFALLESNDIGNCIESSKKIVAFRDGIALMYRAFRSPKMIVLIPTFVLTGVHT
SFWVSIYPTTLTFNSHLSAMIYLPAIYSFGVGLGETTMGLLISFCSKRIKNFGMRPTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIGCELTCLYCALVVISTPPTAPMAPTSEKPLLFQPTRYLVFIIALIGGMSDCCLCSV
RSVVCAIAMPTRRNQAFSVSKFYQAIGCCVIFFISPLLNIYYYVIGIPILCIIASVCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Hypothetical
/protein_id="AAG45570.
/db_xref="GI:12019644"
                                                                                                                                                                                                                 GVMPIGWLIRLTCLTTY"
                                                                                                                                                                                                                                              DGWFDIFGAGEFLPNNWAMKLAAKDICGGLKVEADLCDNVLFLIAGPESDQWNQTRVP
VYATHDPAGTSTQNIVHWMQMVHHGGVPAYDWGTKTNKKKYGQSTTLPLSREPRFTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="coded for by the following
yk788c11.3, yk788c11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FFETRRIKQMEKSLTNMELDQAQQRRRSSKYDTLDEEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis
/strain="Bristol N2"
                                                                                                                                                                 join(5937. .6023,6070. .
7576. .7713,7765. .7881)
                                                                                                                                                                                                                                                                                                    VYYMGHSQGTLTMFSHLSKDDGSFAKKIKKFFALAPIGSVKHIKGFLSFFANYFSLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ZK6.7"
/note="coded for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .6169,6669.
                                                                                                                                                                                           .6169,6669.
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                                                                                                                                                                                           .7138,7228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .7138,7228.
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Mismatches

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Gaps

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Query Match
Best Local Similarity
Matches 16; Conserv
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100.0%; ilarity 100.0%; Conservative (
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join(9204: .9.
10127: .10257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12832..14865
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AHEDLMANYHTSYLDFTIDEVIRINKVDYIRKSQSHQLHFYNMAFHCSTUTPMASSEWHI
SKISPNLENKIRCRLIGRLSELRITDEBYYLLMCVTLIFCNPSLSQLSENGRRLLTSYQH
SKISPNLENKIRCRLIGRLSELRITDEBYYLLMCVTLIFCNPSLSQLSENGRRLLTSYQH
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LNGVGFALYYTGNGGYITSHSTROTIESNVSLSWSFCCCCHIVGSVLMAVITTVTQDQ
IPQLIDAVNVTIGGHGVERREDGEIYLLFSVFAISSAMIFFEMLMPSQDVSNCIEP
SDKVVSFKDGMKLMAETLKSSKMEKLAPTFLLTGMYTAFWSIYPTSLTFNHHNSKMI
YLPAIYGFGVCYGETIMGIIISTLSKRIKDFGLKPTMLIGSVLTTVFCFVALLSTPFD
ATVTPSHEQPLLFQPRRPSYSISDCNNRRNSLGSCFIFFLSPFLNLXHYVIGIPLLCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="contains similarity to C4-type zinc finger (Pfam; zf-C4.hmm, score: 34.58) and to the ligand-binding domai of nuclear hormone receptors (Pfam: hormone_rec.hmm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSFVNLLRFEDQKNLMKEFYIKLTVLINSKQSMSCGKEGMTFPDGSDVLPPTSSEWGI
SKISQNLENKVRCRLIGRLSELRITDEEYLLINFKNFQKFSKILITFSSVFKAFYNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLASNQTCAVCERFTTEFNYGVPSCNACKIFFRRLITRTAPVKQ
CYIGEHCFTKSPITKKCTFCRFQKCIQVGMTLPSYLHFGELTKEKCIDSTIQKLILME
AHRKDLMANYYTSYLNPTIDEVIRLNKVEYTRKSQNHQMSFYNWAFHCCLVTVDFMKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Hypothetical protein ZK6.5"
/protein_id="AAG45580.1"
/db_xref="GI:12019654"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains similarity
zf-C4.hmm, score: 37.95)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14731. .14865)
/gene="ZK6.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Hypothetical protein ZK6.6"
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/db_xref="GI:12019647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGWFD1FGAGEFLPNNWAMKLAAKD1CGGLKVEADLCDNVLFL1AGPESDQWNQTRVP
VYATHDPAGTSTQN1VHWMQMVHHGGVPAYDWGTKTNKKKYGQANPPEYDFTA1KGTK
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VYYMGHSQGTLTMFSHLSKDDGSFAKKIKKFFALAPIGSVKHIKGFLSFFANYFSLEF
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vatDDGYILEMHRIPFGKTNVTWPNGKRPVVFMQHGLLCASSDWVVNLPDQSAGFLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Hypothetical protein ZK6.7a"
/protein_id="AAG45574.1"
/db_xref="GI:12019648"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(17012. .17074,17511. .17607,17658. .18272,18679. .18941)
/gene="zK6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTELSKIVSRKIEKHFQSTKILQIFPEVSSIFQKNLKFSTTFQNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSCILFFRQARQTQVMERKLTQELEESEKRRMAKELEAQMQKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ZK6.6"
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                                                                                                                                                                                                           IKDGMDAAFCN"
                                                                                                                                                                                                                                          LYSSALLQYCLLTYEKAGPARFAELLGICHVIGVQYDDAIHYNVLVQLTKARLDVKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score: 38.56)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11501.
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                                                                                                                        join(20442. .20615,20667. .20801,21151. .21222,21444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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27. .10257,10841.
)1. .11716)
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                              Score 16;
Pred. No.
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341. .11029,11081. .11256,11314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ı protein ZK6.4"
                              1e+02;
                                                                DB 3;
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                                                                Length 40114;
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JOURNAL REFERENCE
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ORGANISM
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AUTHORS
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VERSION
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AC012256/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 18, 2001 this sequence version replaced gi:13357415.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 8, clone RP11-135G15 uppublished
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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SEQUENCE, 18
                                                                                                                                                                                                                                                            Summary Statistics
Sequencing vector: M13; M77815; 69% of reads
Sequencing vector: Plasmid; n/a; 31% of reads
Sequencing vector: Plasmid; n/a; 31% of reads
Chemistry: Dye-terminator Big Dbe; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 163867 bases at least Q40
Consensus quality: 163867 bases at least Q30
Consensus quality: 169031 bases at least Q20
Insert size: 172005; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
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                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.
                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is
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1 1853: contig of 1853 bp in length 1854 1953: gap of 100 bp
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34390 40744: contig of 6355 bp
40745 40844: gap of 100 bp
40845 46688: contig of 5844 bp
46689 46788: gap of 100 bp
46689 55147: contig of 8359 bp
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107720 122838; contig of 15119 bp in length
122839 122938; gap of 100 bp
122939 136635; contig of 13697 bp in length
136636 136735; gap of 100 bp
136736 152497; contig of 15662 bp in length
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152498 173172: contig of 20675 bp in length
173173 173272: gap of 100 bp
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79479 93773: contig of 14295 bp in length
93774 93873: gap of 100 bp
93874 107619: contig of 13746 bp in length
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55248 56028: contig of 9781 bp in length
65029 65128: gap of 100 bp
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27167 30445: contig of 3279 bp in length
30446 30545: gap of 100 bp
30546 34289: contig of 3744 bp in length
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5 3464: gap of
4706: contig c
7 4806: gap of
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79479. 93773
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-354124 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                  SCYOL075C
S.cerevisiae chromosome
Z74817 Y13140
Z74817.1 GI:1419904
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16; Conser
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Direct Submission
Submitted (04-JUL-1996) Data
European yeast chromosome XV
                                                                                                                                                                     Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetaes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 3545)
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                                                                                                                  Unpublished
                                                                                                                                              Alexandraki, D., Katsoulou, C. and Tzermia, M.
                                                                                                                                                                                                                                                                         baker's yeast.
                                                                                                 (bases 1 to 3545)
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50173. .50333
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/db_xref="taxon:10090"
/chromosome="13"
/clone="RP23-354I24"
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XV reading
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collected by MIPS on behalf of the sequencing project. MIPS at the
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| 74 CCTTTCACCAACCCC 1160
                                                                                                                                                                                                                                              l (bases 1 to 4423)
Hocking,D., Webb,E., Radcliff,F., Rothel,L., Taylor,S.,
Pinczower,G., Kapouleas,C., Braley,H., Lee,A. and Doidge,C.
Isolation of recombinant protective Helicobacter pylori antigens
Infect, Immun. 67 (9), 4713-4719 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Conservative
                                                                                                                     2 (bases 1 to 4423)
Hocking,D., Rothel,L., Do
Recombinant Helicobacter
                          Hocking, D.,
                                                                        Unpublished
                                                                                                   predicted to be a 50s
                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori.
Helicobacter pylori
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                                                (bases 1 to 4423)
Submission
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APFFLAYMTLELPLSALASVLYAVFTVLACGLPRTAGNFFATVYCSFIVTCCGERLGI
MTNTFFERPGFVVNCISIILSIGTQMSGLMSLGMSRVLKGFNYLNPVGYTSMIIINFA
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HETKEILQSVNAIFKFGMINALMGPSGGSKSSLLNLISGRLKSSVFAKEDTSGSIMFN
DIOVSELMFKNYCSYVSODDDHLLAALTYKETLKYAAALTHHLTEAERMERTDNLIS
SIGLKHCENNIIGNEFVKGISGGEKRRYTMGVQLLNDPPILLLDEPTSGLDSFTSATI
LEILEKLCREQGKTIITIHQPRSELFKFGNYLLAKSGRTARHGSDEMIAYFTEL
GYNCDSFTNYADFFLDLISVNYONGONEISSRARVEKILSAWKANNDNESLSPTPISE
GYNCDSFTNYADFFLORM
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TFTVLSMGCGFFVNAKVMPVYVRWIKYIAFTWYSFGTLMSSTFTNSYCTTDNLDECLG
NQILEVYGFPRNWITVPAVVLLCWSVGYFVVGAIILYLHKIDITLQNEVKSKQKKIKK
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IMSIHQPRSDILFLLQVCILSKGNVVYCDKMDNTIPYFESIGYHYPQLVNPADYFID
LSSYDSRSMEEAATQSFLNSLIDHMHDYERTHLQLQAEYISNATEIQIQNMTTRIP
FWKQVTVLTRRHFKLMFSDYVTLISTFAEPLIIGTVCGWIYXKPDKSSIGGLRFTTAC
LYASTILQCYLYLLFDTYRLCEQDIALYDRERAEGSYTPLAFIVARKISLFLSDDFAM
                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria; epsilon subdivision; Helicobacter group;
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/note="ORF YOL075c"
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                     Rothel, L.,
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100.0%; Pr
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                     Doidge, C.,
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                  Radcliff, F.,
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                  Lee, A.
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                  and Webb, E
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                                           AE000625 17880 bp
Helicobacter pylori 26695 section
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AE000625 AE000511
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15; Conserv
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ILWEKDTRSGEKNGIKDIKEQSIF IREIPLMTERTSFIINGVERVVNQLHRSPGVIF
KEEESSTSLNKLIYTGQIIPDRGSWLYEEYDSKDVLYARINKRRKVPVTILFRAMDYQ
KQDIIKMFYPLVKVERYENDKYLIPFASLDANQRMEFDLKDPQGKIILLAGKKLTSRKI
KELKENHLEWVEYPMDILINRHLAEPOMVGKEVLDMLTQLDKNKLEKIHDLGVQEFV
IINDLALGHDASIIHSFLADYESLKILKQTEKIDDENALAAIRHKVMKPGDPVTTEV
AKQFVKKLFFDPERYDLTMVGRMKMHKLGLHVPDYITTLTHEDIITTVKYLMKINN
QGKIDDRDHLGNRRIRAVGELLANELHSGLVKNQKTIKDKLTTMSGAPDSLMPHDLVN
SKMITSTIMEFFMGGOLSQFMDQTNPLSEVTHKRRLSALGEGGLVKDRVGETILLFAIQ
EDSHIIAPASTPIDEEGNIGLINTLSTFFRVNDLGFIEAPTKVNDGKVVGETILLFAIQ
EDSHIIAPASTPIDEEGNIGLINTLSTFFRVNDLGFIEAPTKVNDLSSSMLVGVAASLI
PFLEHDDANRALMGTMMQRQAVPLLRSDAPIVGTGIEKIIARDSWGAIKANRAGYVEK
IDSKNIYILGEGKEBAYIDAYSLQKNLRTNQNTSFNOYPIXKGGLVKNGGVLANGAGVI
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786 c 1057 g 1185
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/product="nNA-directed RNA polymerase homolog"
/protein_id="ARA47279.1"
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/translation="MSKKIPLKNRLRADETKTPTDLEVPNLLLLQRDSYDSFLYSKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDRGELALGKNVRVAFMPWNGYNFEDAIVVSERITKDDIFTSTHIYEKEVDARELKHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to C. jejuni
and to E. coli DNA-directed
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LAEEIKNGRIDFDMVIATPDMMAVVGKVGRILGPKGLMPNPKTGTVTMDIAKAVTNAK
SGQVNFRVDKKGNVHAPIGKASFPEEKIKENMLELVKTINRLKPSSAKGKYIRNAALS
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/product="50S ribosomal protein L7/L12"
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/db_xref="GI:1840151"
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Vaggaaabseektefnviladsgaekikvikvvkeitglglkbakdatektphvlkeg
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/protein_id="AAB47277.1"
/db_xref="GI:]840150"
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/strain="Hp921023"
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                            GI:2314349
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                         DB 1;
4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                Length 4423;
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                                                                                                                                                                                                                                                                                                                                               Gaps
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 388 (6642), 539-547 (1997)
97394467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-MAR-1999) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White, 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-AUG-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erratum: [[published erratum appears in Nature 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peterson, J.D., Kelley, J.M., Karp, P.D., Smith, H.O., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori 26695.
Helicobacter pylori 26695
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b, J.-F., White, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 17880)
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                                                                                                                                                                                                                     /gene="HP1190"
complement(1337. .2665)
/gene="HP1190"
                                                                                                                                                                                                                                                                                                    complement(1337. .2665)
                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MKTYNNAIVGASGAVGQELIKGLENSFFPIKKFYPLASTRSAGK
KIKAFNKDYEILETTHEVFEREKIDIAFFSAGGSVSEEFATSASKTALVUNTSFFRL
NKDVPLVVPEINAKEIENAPLNIIANENCSTIQMTQILNFHKIKSVUNTSYSAS
SGAGNKGIESLKNELKTALECLEKDFTIDLNQVLQAGAFAYPIAFNAIAHIDTFKENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(310. .1350)
/gene="HP1189"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(310. .1350)
/gene="HP1189"
                                                                                                                                                              /note="similar to GB:Z11518
PID:32460 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="aspartate-semialdehyde dehydrogenase (asd)"
/protein_id="AAD08235.1"
/db_xref="GI:2314350"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:L08471 SP:Q04797 GB:Z22554 PID:142828
PID:296147 percent identity: 45.67; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Helicobacter pylori 26695"
/strain="26695"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
/product="histidyl-tRNA synthetase (hisS)"
/protein_id="AAD08236.1"
/db_xref="GI:2314351"
                                                                                                                                      similarity; putative"
                                                                                                                                                                                                                                                                                                                                        ALKIALHYIKNA"
                                                                                                                                                                                                                                                                                                                                                                  APSVAVCDDPSHNLYPTPLKASHTDSVFIGRLRKDLFDKKTLHGFCVADQLRVGAATN
                                                                                                                                                                                                                                                                                                                                                                                               YTKEELKMLHETHKIMGVDFPISATCVRVPVLRSHSESLSIAFEKEFDLKEVYEVLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:85962"
                                                                                  /transl_table=11
                                                                                                         /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .17880
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                                                                                                                                                                 GB:X05345 GB:M96646 SP:P12081 32.39; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kirkness, E.F.,
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                                                                                                                                                                                                                     transl_table=11
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LEYAQTLLPDASSDIQKEIYRFKDHGDRDVALRFDLIYVPLARRVSLHIQTLGMPFKRY
AIGNVERGERAQKGRYRBFYGCDFDFIGSESLVCDAEIIQVIVASLKALDLEDFOVSI
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putative" 'note="hypothetical protein; identified by GeneMark; /gene="HP1194"

coding region HP1194"

complement(5999. .8077) /gene="HP1195" complement(5999. /gene="HP1195" /product="H. pylori predicted /protein_id="AAD08244.1" /db_xref="GI:2314359" /translation="MLFKNPLIHRPPYKKFRLTNDKLFCIQS complement(5999. .8077)

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16078 CTTTCACCÁACCCCC 16092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
15; Conser
                                                                              Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
Muzny, D.M., Adams, C., Adio-Oduola, B.,
                                                                                                                                                                                         AC107593.1 GI:18266586
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                              AC107593
                                                                                                                                                                                                                                                                                                      Rattus
                                                          Kattus.
                                                                                                                                                                                                                                                                                                                             AC107593
                                                                                                                                                                     Norway rat
                            (bases 1 to 26236)
                                                                                                                                                                                                                                                                       us norvegicus clone CH230-18605, 17 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mkrrkapvrevlgdpvygnkvvtkfinkmmfdgkksvaekiiyk
afnkieeksgekgievfekalervrplvevrsrrvggatyqvpvevrasrqqslsirw
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VSVFCSVGGVQPQSETWWQANKYGVPRIVEVEWMDRIGANFYXDYENQIKLRIKANPV
PINIPIGAEDTPIGVIDLVQMKAIVWNNETMGAKYDVEBIPSDLLEKAREVREKLVEN
VAEQDEALMEKYLGGEELSIEEIKKGIKAGCLNMSLVPMLCGSSFKNKGVQTLLDAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="translation elongation factor EF-G (fusA)'/protein_id="AAD08239.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(8572. .8979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="ribosomal protein S7 (rps7)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(8089. .8556)
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YDGSYHDVDSSEMAFKIAGSMAFKEASRAANPVLLEPMMKVEVEVPEEYMGDVIGDLN
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LESGSYVYNSTKDKKERVGRLLKMHSNKREDIKEVYAGEICAFVGLKDTLTGDTLCDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNSALRKVAKVRLTSKFEVISYIPGEGHNLQEHSIVLVRGGRVKDLPGVKYHIVRGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="ribosomal protein S12 (rps12)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to SP:P18662 percent identity:
identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MPTINQLIRKERKKVVKKTKSPALVECPQRRGVCTRVYTTTPKK
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                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
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5. *** SEQUENCING
Ali-osman, F.R., Allen, C.
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JOURNAL REFERENCE

TITLE

AUTHORS TITLE

JOURNAL

COMMENT

CDS

CDS gene

REFERENCE AUTHORS

SOURCE KEYWORDS

ORGANISM

* NOTE: Estimated insert size may differ from sequence length
. (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is

Consensus quality: 21752 bases at least Q40 Consensus quality: 23932 bases at least Q30 Consensus quality: 25882 bases at least Q30 Consensus quality: 25882 bases at least Q20 Estimated insert size: 18630; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation

findPhrapList

* arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown

VERSION ACCESSION DEFINITION AC107593 RESULT

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Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonin, D., Bouck, J., Bouck, J., Blowie, S., Briewa, M., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, R., Chen, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Cox, C., Cleyeland, C.D., Cox, C., Chen, R., Chen, P., Chen, R., Chen, P., Chen, Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Worley, K.C. Direct Submission Unpublished
2 (bases 1 Direct Submission (bases 1 to 26236) Sequencing vector: Plasmid; M77789
Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye: 98% of reads
Assembly program: Phrap; version 0.990329First call to Center project name: GOVS Center clone name: CH230-18605 Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/

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RESULT 11
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AUTHORS
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2 (bases 1 to 26458)
2 (bases 1 to 26458)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boutwell,C.,
Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S.,
                                                                                                                                                                                                                                                                                                         l Similarity
15; Conserv
                                                                     ngalumiars, .... 26458)

1 (bases 1 to 26458)

Birren, B., Linton, L., Nusbaum, C., Page, D. and Lander, E.

""" "anians chromosome Y, clone hCIT. 298_B_15
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                  AC005942
                                                                                                                                                                                             Homo sapiens chromosome
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/organism="Rattus norvegicus"
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/clone="CH230-18605"
4887 c 4901 g
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                                                                                                                                                                      GI:4263846
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Locus

Submitted (06-JUN-2000) Whitehead Institute/MIT Center for Genome

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Vassilev, H., Y.,...

Ye, W.J. and Zody, M.

Direct Submission

AL Submitted (13-0CT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Streen, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,

Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,

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Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L.,

Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P.,

Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,

Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,

Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,

Skaletsky, H., Stange-Thomann, N., Stojanovic, N., Stone, C.,

Subramanian, A., Sun, C., Tesfaye, S., Torruella-Miller, I.,

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Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
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Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,
Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
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J., Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Paviin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W. J., Zhao, J. and Zody, M.
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Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D.,
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M. Barren,B., Linton,L., Barna,N., Beckerly,R., Benn,J., Brown,A., Castle A. Cerny, T. Olargaen M. Collings C. Collings A. Castle A. Cerny, T. Olargaen M. Collings C. Castle A. Cerny, T. Olargaen M. Collings C. Castle A. Castle A.
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on Feb 24, 1999 this sequence version replaced gi:4225939.
All repeats were identified using RepeatMasker: Smit, A.F.A.
Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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/note="%3ingle-stranded complement(792..1106)
/rpt_family="%AluSq"
complement(1107..1392)
/rpt_family="LTR9"
                   /rpt_family="MER4B-internal"
6455. .6625
                                                       /rpt_family="MER4D" 6085. .6454
                                                                                           /rpt_family="MER50"
5792. .6033
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complement(4298. .4393)
/rpt_family="MER4A"
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/rpt_family="MER4A"
complement(4045. .4270)
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complement(2099. .2400)
/rpt_family="AluSx"
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/rpt_family="AluSp"
complement(737..791)
/rpt_family="LTR9"
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4927. .5229
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complement(4908. .4926)
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4739. .4907
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4271. .4297
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complement(3715..3974)
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/rpt_family="MER72"
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complement(2734. .2921)
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complement(#0.4
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complement //'"
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/clone_lib="CITC Human BAC"
 rpt_family="MER4-internal"/
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/db_xref="taxon:9606"
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TITLE
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HS212J10
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Best Local Similarity 100.
Matches 15; Conservative
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           Submitted (05-JAN-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 29, 1998 this sequence version replaced gi:4007136.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with noily a small overlap as described above.
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                   Human DNA sequence from clone 212J10 on chr. Contains ESTs and a GSS, complete sequence. AL034401
                                                                                                                                                                                                                                                                                                                                   HTG.
IMPORTANT: This sequence is not the entire insert of clone 212J10
                                                                                                                                                                                                                      Grafham, D.
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9152. .9425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(12784..12954)
/rpt_family="AluSg/x"
complement(13050..13226)
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11376
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7475. .7577
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11961
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11425
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7156. .7355
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Pred. No. 4.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is 
feature key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The true left end of clone 448E20 (297196) is at 30109 in this sequence. The true right end of clone 417G15 (AL009174) is at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It may be shorter because we only sequence overlapping once, or longer because we arrange for a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212J10 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2551. .2745 of
complement(2474. .2892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSx repeat: matches 1.
8688. .8859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluY repeat: matches 2. 6908. .7088
                      /note="MSTB repeat: matches 1.
17435. .17491
                                                                                                                                                                                                                                                                                                      /note="L2 repeat: matches 2584.
12097. .12126
/note="10 copies 3 mer aac 100%
12665. .12972
/note="AluSq repeat: matches 3.
                                                                                                                                                                                              /note="MER5B repeat: matches 12.
14161. .14346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="MIR repeat: matches 201.
                                                                  16805
                                                                                                              /note="MIR repeat: matches 20.
16380. .16697
                                                                                                                                                                                                                                            14015
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER45 repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="match: GSS B95157"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSx repeat: matches 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L2 repeat: matches 2515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP1-212J10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="q25-26.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                  'note-"AluSq repeat: matches 1.
                                                                                                                                                                                                                                                               note="26 copies 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match: ESTs R94487 AI022438"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 5993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .9149
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                                                                                                                                                                                                                                                                                          .13770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIR repeat: matches 19. .134 of consensus"
                                                                                                                                                       . 15553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 repeat: matches 2495.
                                                                                                                                                                       repeat: matches 1629.
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                                                                                                                                                                                                                                                                 mer
                                                                                                                                                                                                                                                                 ca 87% conserved"
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                                                                                                                              .261 of consensus"
                                           .426 of consensus"
                                                                                                                                                                                                                                                                                                                                                    conserved"
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.255 of consensus"
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nes 15; Conserv
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         Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Blimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Chen, R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Hartis, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Tachson, B., Tia, Y., Hohson, B., Toliger, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTTTCACCAACCCC 1982
                                                                                                                                                                                                                                                                                                                                                                       Muzny, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus clone CH230-1D24,
Jackson,L.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norway
                                                                                                                                                                                                                                                                                                                                                                                                                Rattus
                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 46363)
ny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 15; DB 9; L
ilarity 100.0%; Pred. No. 4.3e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L2 reror
28750
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/note="MER5A repeat: matches 3.
18324. .18488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: 6309 c 5771 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29510. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSx repeat: matches 1.
25794. .26104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21170.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="41 copies 2 mer tt 76% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MER94 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="Alu repeat: matches 268.
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  Jia,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matches 12.
8899 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8. .124 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _Length 30208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .215 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .1604 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .261 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .307 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .134 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K., Wu, C., Wu, Y., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary.
                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid; M77789

Chemistry: Dye-terminator Big Dye: 99% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 19414 bases at least Q40

Consensus quality: 2250 bases at least Q30

Consensus quality: 24040 bases at least Q30

Consensus quality: 24040 bases; estimation

Duality coverage: 0x in Q20 bases; sum-of-contigs estimation

Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: TUFM Center clone name: CH230-1D24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: BCM
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                                                                                                    of 890 bp in length unknown length
                                                                                                                                                                                                           unknown length of 946 bp in length
                     of 944 bp in length unknown length
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of 909 bp in
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                                                                                   /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-1D24"
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                                                                                                                                                                        Location/Qualifiers
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32: gap of unkn...

61: contig of 1429 bp ...

661: gap of unknown length

7927: contig of 266 bp in length

1927: gap of unknown length

19429: contig of 1402 bp in length

19529: gap of unknown length

20481: contig of 952 bp in length

20581: gap of unknown length

21432: contig of 851 bp in length

21532: gap of unknown length

21532: gap of unknown length

21815: contig of 1283 bp in length

21815: contig of 1283 bp in length

21815: contig of 1313 bp in length

21815: contig of 1313 bp in length

21815: contig of 1313 bp in length
                                                                                                                                                                                   37480: gap of unknown length
38539: contig of 1059 bp in length
38539: gap of unknown length
40233: contig of 1596 bp in length
40335: gap of unknown length
41516: contig of 1181 bp in length
41610: gap of unknown length
42512: contig of 896 bp in length
42612: gap of unknown length
426171: gap of unknown length
43771: contig of 1159 bp in length
43871: gap of unknown length
43871: gap of unknown length
45209: contig of 1338 bp in length
45309: gap of unknown length
45309: gap of unknown length
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10077: contig of 901 bp in
10177: gap of unknown lengt
11122: contig of 945 bp in
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of 922 bp in
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of 897 bp in 1
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Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
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Mlenga, V., Murphy, T., Naylor, J., Myuyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tonham, K., Travers, M., Talamas, J., Tesfaye, S., Theodore, J.,
* NOTE: This record contains 79 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J. Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Ve, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center clone name: 317_B_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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LOW-PASS SEQUENCE SAMPLING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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10976: contig of 706
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11767: contig of 691
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132: gap of 100 b

14118: contig of 686
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1431: co
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18048: contig of 705 b
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28413: contig
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27612: contig of 713
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22784: contig of 683
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Benton, J., Blande, K., Blankenburg, K., Bonnin, D., Bouck, J.,
Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N. P., Buhay, C.,
Burch, P., Burkett, C., Burrell, K.L., Byd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, G.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Deavy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Delan, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.
Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J.,
Foster, P., Frantz, P., Gablsi, A., Gao, J., Garcia, A., Garner, T.,
Foster, P., Frantz, P., Gablsi, A., Gao, J., Garcia, A.,
Garrer, M., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
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Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
J., Martinez, E., Massey, B., Mawhiney, E., McLeod, M.P., Meaton, N.,
Morgan, M., Morris, S., Moser, M., Oviedo, N., Newtson, J., Nohabbat, K.,
Martinez, E., Massey, B., Mawhiney, E., McLeod, M.P., Meator, M.,
Morgan, A., Nguyen, N., Nickerson, E., Nwokenkov, S.,
Oguh, M., Okcuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
Quiles, M., Ren, Y., Rives, M., Sott, R., Molbokan, I., Rolfe, M.,
Sisson, I., Sodergren, E., Sonake, T., Sparks, A., Stanley, H.,
Shomas, N.,
Tanger, J., Taylor, C., Taylor, P., Telfrod, B., Thomas, N.,
Tanger, J., Warder, L., Washer, V., Villadon, D., Vinson, R.,
Wolles, W., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
                                                                                                                                                                                                                                                                                                                                            Submitted (23-OCT-2001) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:17062261.
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Center clone name: CH230-103F13
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                                                                                                                Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
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findPhrapList
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NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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H. pylori GHPO 741
Helicobacter pylor
Soybean 240017 reg
Soybean 240017 reg
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                    WPI; 1985-007981/02
                                                              Shine J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to manipulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
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RESULT 3
AAX13959/c
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AC AAX13959;
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KW Peptic ult
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AAX1959;
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AAX1959;
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1997;
01-APR-1997;
24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         When this gene is expressed in a Rhizobium sp., the bacterium produces useful products and plants may have their properties improved, e.g. the rate, quality and efficiency of the nitrogen-fixation process, especially in the root nodules of Rhizobium strains. See also AAN50526-7 and AAP50773-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHPO protein;
peptic ulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. pylori GHPO 741 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial strain contg. recombinant DNA Rhizobium strains for improved nitrogen
                                                                                                                                                                                                                                                                                                                                Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1999
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                                                                                                                                                                                  isolated Helicobacter polynucleotides - the diagnosis, prevention and treatment actions and gastrointestinal diseases
                                                                                                                                                                                                                                                                       1998-542293/46.
DB; AAW98240.
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15; Conser
                                                                                                                                                                                                                                                                                                                                                                         MERIEUX ORAVAX PASTEUR MERIEUX
                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME SCI INC
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                                                                                                                                            Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 5;
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97US-0833457.
97US-0881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US06371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 49..3030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               improved nitrogen
                                                                                                                                            2054pp;
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                                                                                                                                            English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gastroduodenal disease;
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2.1e+02;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fixation
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                                                                                                                                                                                                           Helicobacter
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                                                                                                                                                                                                                                                                                                                                J,
                                                                                                                                                                                                                            products
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This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peging for the protein the second content of the second conten

ulcer diseases,

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RESULT 4
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23-OCT-2000;
27-NOV-2000;
                                                                                             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The autisense nucleic acids can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1711 CTTTCACCAACCCCC 1697
                                                                                                                                                                                                                                     New polynucleotides antibiotics, compris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for the production of antibodies. detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS53676 standard; DNA; 8673
          to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.
                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                        WPI; 2001-611495/70
                                                                                                                                                                                                                                                                                                                  Yamamoto
                                                                                                                                                                                                                                                                                                                                Haselbeck
                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS53676;
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15; Conservative
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                                                                                                                                                                                                                                                                                                                 RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; prokaryotic cellular pro
; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                            2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                      comprise
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                                                                                                                                                                                                                                                                                                                 Ohlsen
Xu HH;
                                                                                                                                                                                                                ID No 7313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                      for the identification and development se sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.8%;
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Pred. No.
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,. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          814
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not
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                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhgl or an Rhg4 SCN resistant allele. The nucleic acids can be used for investigating rhgl or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into sowbean plants and for introgressing SCN resistance or partial SCN resistance into sowbean plants and for introgressing SCN resistance or partial SCN resistance into sowbean plants and for introgressing SCN resistance or partial SCN resistance into sowbean plants and for introgressing SCN resistance or partial 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soybean; antihelmintic; gene therapy; soybean cyst nematode; SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breec 240017 region G3; 318013 region A3; 515002 region G2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                  resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins. The present sequence is a nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified nucleic acid for producing a soybean plant having soybean cyst nematode resistance and for use in plant breeding programs - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hauge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001
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                                                                                                                                     Sequence 335913 BP; 114579 A; 53403 C;
                                                                                                                                                                                                      provided
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DB; AAM42214.
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15; Conser
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                                                                                                                                                                                                      the specification.
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Score 15;
Pred. No.
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Pred.
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3. 2.3e+02;
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DB 22; I
                                                                                                                                        53026 G;
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                            Length 335913;
                                                                                                                                        114905 T;
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RESULT 7
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AAI61372/c
ID AAI613
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                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                      291134
           Human secreted protein-encoding
                                                                                                                                                                                                                                                                                         The nucleic acids can be used for investigating rhyl or Rhy4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins. The present sequence is a nucleic acid molecule provided in the specification.
                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acid molecules from regions of the soybean genome, which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhg1 or an Rhg4 SCN resistant allel
                                      17-JUL-2001
                                                               AAD05460;
                                                                                       AAD05460 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New purified nucleic acid for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAM42215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hauge BM, Wang ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-2001; 2001WO-US00552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soybean; antihélmintic; gene therapy; soybean cyst nematode; SCN; sCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding; 240017 region G3; 318013 region A3; 515002 region G2; ds.
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                                                                                                                                                                                                                                                                     Sequence 335913
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                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                       Conservative
                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resistance
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                                                                                       cDNA; 347
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             gene
                                                                                                                                                                                                       Mismatches
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             22 cDNA clone HT4ES80,
                                                                                                                                                                                                                                                                     53027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a soybean plant having soybean plant breeding programs -
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             SEQ ID NO:82
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amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 29 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzhelmer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                    healing and epithelial cell proliferation, to prevent skin aging due to
sunburn, to maintain organs before transplantation, for supporting cell
culture of primary tissues, to regenerate tissues, to identify their
                                                                                                                                                                AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, britishionis disease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 29 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound
                                                                                                                            skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders,
                                                                                                                                                                                                                                                                                                                                                               The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                           AAD05389-AAD05473 represent cDNAs corresponding to 29 human secreted protein genes, and AAE01546-AAE01630 represent the proteins they encode. AAE01631-AAE01660 represent human secreted protein fragments or variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1999; 99US-0163577
30-JUN-2000; 2000US-0215137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding partner identification; chromosome 16; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               foetal abnormality; developmental abnormality; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-316490/33.
DB; AAE01617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Komatsoulis
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4..210
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/transl_except= (pos:58..60, aa:Xaa)
/transl_except= (pos:178..180, aa:Xaa)
/note= "Xaa corresponds to any of the naturally occurring
L-amino acids; CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/product= "Mature human secreted protein"
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tissues,
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RESULT
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AAI83975 :
                                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny, inhibin activity and may be useful in the diagnosis and/or activity factor activity and may be useful in the diagnosis and/or activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human
          Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                WPI; 2001-514838/56
                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000;
18-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide
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                                                            treatment of cancer,
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                                                            leukaemia,
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14-JUL-2000

26-JUL-2000

26-JUL-2000

14-AUG-2000

14-AUG-2000
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; neuroprotective; cytostatic; dermatological; viru immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulne antiparkinsonian; antistkling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccin
                                                                                                                                                                                                                                                                                    07-JUL-2000;
11-JUL-2000;
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19-MAY-2000;
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17-MAR-2000;
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15; Conser
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              2000US-0180628.
2000US-0186350.
2000US-0189874.
2000US-0198123.
2000US-029815.
2000US-029815.
2000US-0298164.
2000US-02119135.
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2000US-0217486.
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2000US-0217487.
2000US-0225964.
2000US-0225913.
2000US-0225267.
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2000US-0225447.
2000US-0225475.
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2000US-0225758.
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30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 05-SEP-2000 06-SEP-2000

08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 12-SEP-2000

14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

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                                                                                                                                                                The invention relates to novel genes (ABA11004-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. CT whe nucleic acids, proteins, antibodies and (ant)agonists are useful CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (C) cardiovascular disorders such as myocardial ischaemias; (C) cardiovascular disorders such as myocardial ischaemias; (C) cardiovascular disorders such as viral, bacterial, fungal CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly control of the printed specification, but was obtained in electronic format directly control of the control of the printed specification, but was obtained in electronic format directly control of the control
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17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
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nes 15; Conservative
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DB; ABB14980.
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2000US-0249245

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                                                                                           Score 14.4; DB Pred. No. 4e+02;
                                                                                                                                                                86 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + Sequence Listing; English.
                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nervous system antigen polypeptides, and/or treating nervous system
                                                                                                                                                                144 T; 5 other;
                                                                                                            22;
                                                                        1:
                                                                                                            Length
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29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

2000US-022994.
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2000US-02394.
2000US-02394.
2000US-023124.
2000US-023124.
2000US-023124.
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2000US-023196.
2000US-023306.
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2000US-02360.
2000US-02360.
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2000US-02360.
2000US-02360.
2000US-0241786.
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2000US-024180.
2000US-024180.
2000US-024180.
2000US-024661.

14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000

02-OCT-2000
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13-OCT-2000
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00-NOV-2000
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00-NOV-2000
00-NOV-2000
01-NOV-2000

AAK70540 standard; DNA; 736 BP

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RESULT 10
AAS64618/c
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                                                                                                                                                                                          CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, are also used in diagnostics as expressed sequence tags of cridentifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or cridentiating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical company of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations company in the produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed content of the variation, but was obtained in electronic format directly from WIPO at fra. wino. intranhombitished not sequences.
                                                                                  Query Match
Best Local :
                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS64618
                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 422; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABG00431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
532
                                                                Local Similarity 93.1 hes 15; Conservative
                                1 cctttcaccaaccccc 16
                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
CCTTTCACCAATCCCC
                                                                                                                                                    606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; cDNA;
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                                                                                                                                                    B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                    128
                                                                                  90.0%;
                                                                                                                                                  Α;
                                                                                                                                                    188
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                                                                                  Score 14.4; DB Pred. No. 4e+02;
                                                                                                                                                  133 G;
                                                                  Mismatches
                                                                                                                                                    157
                                                                                                                                                  T; 0
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                                                                1;
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                                                                                                Length
                                                                Indels
                                                                                                  606;
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                                                                Gaps
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RESULT

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AAK70540/C

AAK70540/C

XX

AC AAK705

XX

AC AAK705

XX

Human

XX

CyCost

XX

W02001

XX

W02001

XX

W02001

XX

W02001

XX

O9-AUG

XX

FR

04-FEB

PR

07-UIL

PR

11-AUG

PR

11-AU
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20-JUL-2000
20-JUL-2000
21-JUL-2000
21-AUG-2000
11-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune; haematopoietic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0225213
2000US-0225214
2000US-0225266
2000US-0225267
2000US-0225268
2000US-0225270
2000US-0225270
2000US-0225447
2000US-02254757
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2000US-0215135.
2000US-0216647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0179065
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2000US-0224519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0184664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune/haematopoietic antigen; cancer;
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20-OCT-2000

20-OCT-2000

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01-NOV-2000

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02-OCT-2000;
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29-SEP-2000;
02-OCT-2000;
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27-SEP-2000;
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21-SEP-2000;
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13-OCT-2000;
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29-SEP-2000;
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25-SEP-2000;
2000US -0233055
2000US -0234274
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2000US -024677
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2000US-0232399.
2000US-0232400.
2000US-0232401.
2000US-0233063.
2000US-0233064.
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$\times CCCCCCCCCCCCCCCX\times \times \times
                                                         AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and C treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome C that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK64922 to AAK84950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-2000;

05-DEC-2000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding useful for preventing,
Sequence 736 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
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2000US-0251879
2000US-0251856
2000US-0251869
2000US-0251869
2000US-0251989
2000US-0251989
2000US-0251989
2000US-0254097
2000US-0254097
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   218
   c;
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   192
   ç;
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   Τ,
   0 other;
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멍
                                 Matches
                                        Query Match
Best Local
571 CCTTTCCCCAACCCCC 556
        1 cctttcaccaaccccc 16
                                l Similarity
15; Conserv
                                 Conservative
                                         93
                                        . 88;
                                  0
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Pred. No. 4.1e+02;
0; Mismatches 1;
                                                Length
                                  Indels
                                                 736;
                                 0;
                                 Gaps
                                  0,
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DNA;

736

(first entry)

Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25353.

RESULT 12
AAK70541/c
ID AAK70541;
XX
AC AAK70541;
XX
C AAK70541;
XX
DT 06-NOV-2001 (first 6
XX
DE Human immune/haemator
XX
Human; immune; haemat
XX
Human; immune; haemat
XX
Human; one thei
XX
Human; one cytostatic; gene therapy; vaccine; Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; metastasis;

17-JAN-2001; 2001WO-US01354.

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31-JAN-2000
24-FEB 2000
24-FEB 2000
24-FEB 2000
11-MAR-2000
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28-JUN-2000
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תקרום להודים להודים
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02-OCT 2000
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08-NOV 2000
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09-NOV
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useful f
                                                WPI;
                                                2001-483426/52
                                                                             CA,
for preventing, diagnosing and/or treating
                                                                                                                                     2000US-0236802

2000US-0237038

2000US-0237039

2000US-0237039

2000US-0241786

2000US-0241786

2000US-0244617

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2000US-0250391

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   antigen polypeptides, cancers and
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RESULT 13
AAK70542/c
ID AAK70542 standard; DNA; 736
            TARRES PRESENTATION OF THE PROPERTY OF THE PRO
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Best Local S
Matches 15
     31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
11-AAR-2000;
11-AAR-2000;
11-AAR-2000;
19-MAY-2000;
07-JUN-2000;
07-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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11-JUL-2000;
14-JUL-2000;
14-JUL-2000;
14-JUL-2000;
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cytostatic; gei
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15; Conservative
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     2000US-0179065
2000US-018628
2000US-0184664
2000US-0188350
2000US-0189874
2000US-0199074
2000US-0199075
2000US-029515
2000US-0205515
2000US-0214886
2000US-021647
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2000US-0217487
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vaccine; metastasis; ds.
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Pred. No. 4.1e+02;
0; Mismatches 1;
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     14-SEP-2000;
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21-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
29-SEP-2000;
21-CCT-2000;
21-CCT-2000;
22-CCT-2000;
22-CCT-2000;
23-CCT-2000;
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25-CCT-2000;
26-CCT-2000;
27-CCT-2000;
28-CCT-2000;
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20-CCT-2000;
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01-SEP-2000
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14-SEP-2000;
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2000US-0231243
2000US-0231413
2000US-0231413
2000US-0232081
2000US-0232081
2000US-0232081
2000US-0233296
2000US-0233399
2000US-0233400
2000US-0233400
2000US-0233401
2000US-0233403
2000US-02334724
2000US-02334274
2000US-02342997
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2000US-0229513

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2000US-0231242
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2000US-0225268.

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2000US-0225447.

2000US-0225757.

2000US-0225758.

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2000US-0226681.
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2000US-0227182
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amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) coplynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent. CC diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
                                                                                                                                                                                 AAK54951 to AAK64702 encode the human immune/haematopoietic antigen
                                                                                                                                                                                                            Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                             Nucleic
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2000US-0246653

2000US-0246610

2000US-0246611

2000US-0249207

2000US-0249207

2000US-0249209

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2000US-0249210

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2000US-0256719.
2000US-0251479.
2000US-0251868.
2000US-0251869.
2000US-0251869.
2000US-0251869.
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2000US-0249300.
2000US-0250160.
2000US-0250391.
2000US-0251030.
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2000US-0246478
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cancers antigen

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Best Local
                                                                          The invention relates to human breast cancer expressed polynucleotides (AALO7544-AALZ6789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and polypeptides are also useful for isolating compounds with cytostatic polypeptides are also useful for isolating compounds with cytostatic
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29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                      Claim 1;
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14-MAR-2000;
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2000US-0189167.
2000US-0192099.
2000US-0193480.
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Score 14.4; DB 22
Pred. No. 4.1e+02;
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RESULT 15
AAH07529/s
AAH07529;
XX
AAH07529;
XX
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AAH07529;
XX
DT
26-JUN-2001 (first entry)
XX
DE
Human cDNA clone (5'-primer) diagramer, detection; describer, detection; descr
   Matches
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Best Local
                                                                                                                                                                                                                        sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13633 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes primer sets for synthesising 5602 full-length cpNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynuclectides, particularly the 5602 full-length chars defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length chars -
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Sugiyama T, Wakamatsu A, Nagai K,
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BH557406 BGGJOS6TR
BG771897 602721709
AZ210049 SP_0153_A
AZ299798 RPCI-23-4
AZ019845 RPCI-23-2
BM106270 509959 MA
A1991910 ws42c04.x
A0880479 HS_5044_A
BE347738 sp02g09.y
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RESULT BB430167 LOCUS VERSION ACCESSION DEFINITION BB430167 218 bp mRNA linear EST 18-JUL-20 BB430167 RIKEN full-length enriched, adult male hippocampus Mus musculus cDNA clone C630031019 3' similar to X86406 R.norvegicus mRNA for brevican, GPI-anchored isoform, mRNA sequence. EST BB430167.1 GI:9269894 EST 18-JUL-2000

ALIGNMENTS

KEYWORDS SOURCE ORGANISM REFERENCE Mus musculus Mammalia; house mouse.

AUTHORS mmalia; Eutheria; (bases 1 to 218) Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shipata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, R., Watanatsu, M., and Hayashizaki, Y., Kiten Mouse ESTs (Konno, H., et al.)

TITLE JOURNAL

COMMENT

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by

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RESULT 2
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 445)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Peterston, R. and Wilson, R. The Washor, R. and Wilson, R. The Washor, R. and Wilson, R. Waterston, R. and Wilson, R. Washor, C. Mouse EST Project 1999

Unpublished (1999)

Contact: Marra M/Washu-NCI Mouse EST Project 1999

Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                          A1452374 445 bp mRNA linear EST (mq89907,x1 Stratagene mouse heart (#937316) Mus musculus IMAGE:585948 3', mRNA sequence.
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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Itoh.M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTTAATTTAATTTAATCCCCCCCCCCCC 3']" a 73 c 31 g 62 t
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/dev_stage="adult"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C630031019"
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 564.
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Location/Qualifiers
                                                                                                                                      84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi A., Barber, M., Beacorn, T., Duval, Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Ped, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZB71533 564 bp DN
2M0184N21F Mouse 10kb plasmid UUGC1M
Clone UUGC2M0184N21 F, DNA sequence.
                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ871533
                                                                                                                                                                                                                                                                                 plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ871533.1 GI:13077828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
l (bases 1 to 564)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus
/strain="NIH/Swiss"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:585948"
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Pred. No. 2.4e+03;
Mismatches 0;
                                                                                                   Std Error:
                                                                                                                                                                                                                                                                                                                                                     Beacorn,T., Duval,B., Hamil,C.,
,M., Meenen,E., Pedersen,T., Reilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse heart (#937316)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library Mus musculus
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Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Wagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; brassica.
                                                                                                                                                                                                                                                                                                                                                  Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOGJO56TF
                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 796)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH557406 796 bp
BOGJO56TR BOGJ Brassica oleracea
                                                                                                                                                       Class: sheared ends
                                                                                                                                                                                                                                                                                                                                  Contact: Chris Town
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                                                                                                                                                                                              il: cdtown@tigr.org
is from a doubled haploid
                                                                                                                                                                                                                                        Medical Center Drive, 301-838-3523 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114|gb|AFT29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
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123 c 103 g 195 t
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                    /db_xref="taxon:3712"
/clone="BOGJ056"
                                                                /organism="Brassica oleracea"
/strain="TO1000DH3"
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/clone="UUGC2M0184N21"
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/strain="C57BL/6J"
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                                                                                                                            Location/Qualifiers
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Pred. No. 2.4e+03;
; Mismatches 0;
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BG771897/c
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RESULT 4 BH557406/c

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16;

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678 CCTTTCACCAACCCCC 663
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                                       1 cctttcaccaaccccc 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10772 row: b column: 03
High quality sequence stop: 837.
Location/Qualifiers
1 027
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16; Conser
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BG771897.1 GI:14082550
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602721709F1 NIH_MGC_97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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1 (bases 1 to 837)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4838306"
/clone=lib="NIH_MGC_97"
/lab_host="DH10B"
                                                                                                                                                                                                                               /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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Pred. No. 2.4e+03;
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Pred. No. 2.4e+03;
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RPCI-23-439C15.TV RPCI-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrotus purpuratus Eleutherozoa; Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SP_0153_Al_H11_T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone plate=153 Col=21 Row=O, DNA sequence.
                                                                          1 (bases 1 to 190)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J.,
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 1024.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 153 row: 0 column: 21
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               additional resources
Unpublished (1999)
                  Mouse BAC End Sequences from Library RPCI-23
                                    and Fraser, C.M.
                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                 AZ299798.1 GI:9541583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: acameron@caltech.edu
Plate: 153 row: O column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U. S. A. 97 (17),
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                                                                                                                                                                                                                                                   DNA sequence.
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ilarity 100.0%;
Conservative (
                                                      Levins, M., Mcgann, S.,
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/db_xref="taxon:7668"
/clone="plate=153 Col-21 Row=0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Strongylocentrotus purpuratus, purple
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Pred. No. 2.4e+03;
); Mismatches 0;
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                                                                                                                                                                                                                                                                         musculus
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JOURNAL
                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTTTCACCAACCCC 95
                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea Ch Genetics (lifo@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 439 row: C column: 15
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong
                                                                                                                                                                                               Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 246)
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                             Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                          and Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A2019845.1 GI:7095229
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                                                                                                                                                                                                                                                                  В.,
                                                                                                                                                                                                                                                                                                                                                                                              house mouse
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                                          szhao@tigr.org
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/strain="C57BL/GJ"
/db_xref="taxon:10090"
/clone="RPCI-23-439C15"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ; Kidney/Brain; Vector: pBACe3.6; Site_1: /note="Organ; Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI wethylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into EcoRI sites.
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6.4e+03;
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TITLE
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                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd, ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA503034 329 bp mRNA linear EST 19-AUG-199 nh58b03.s1 NCI_CGAP_Pr8 Homo sapiens cDNA clone IMAGE:956525 similar to gb:D10667 MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (HUMAN);contains element PTR7 repetitive element; mRNA sequence.
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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/clone="RPCI-23-294J24"
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/tissue_type="prostate"
                                                                           /clone="IMAGE:956525"
                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                        Location/Qualifiers
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                                                 /clone_lib="NCI_CGAP_Pr8"
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1 (bases 1 to 353)

Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K. Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998) Other_GSSs: RPCIll-17C17.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS.
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RPCI11-17C17.TP RPCI-11 Homo
                                                                                                                                                                                                                                                                                                                                      Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                       library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 838 0200 Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                       http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                        Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pAMP10; mRNA made from invasive prostate tumor, cDNA made by oligo-dT priming. Non-directionall cloned. Size-selected on agarose gel, average insert size 600 bp. "
                                                                                                            /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
60 c 65 g 126 t
                                                                                                                                                                                       /sex≈"Male"
                                                                                                                                                                                                      /clone_lib="RPCI-11"
                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="RPCI-11-17C17"
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="GDB:7506208"
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Pred. No. 6.5e+0;
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clone RPCI-11-17C17,
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                                           AV212743 380 bp mRNA linear EST 30-OCT-1999
AV212743 RIKEN full-length enriched, ES cells Mus musculus cDNA
clone 2410118E09 3' similar to D85818 Mouse mRNA for RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL2-CS0048-221100-249-D11 CS0048 Homo sapiens CDNA, BF766646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dias Néto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstéin,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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      II subuunit RPB14, mRNA sequence.
AV212743
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221100-249-D11&t3=2000-11-22&t4=1)
Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: colon_est; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                              tissue mRNA and cDNA amplification
low stringency conditions."
101 c 62 g 112 t
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/clone_lib="CS0048"
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The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carrinci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yoshihide Hayashizaki
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                                  105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                       prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5]
                           prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="2410118E09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="ES cells"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Site_1: XhoI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kanagawa 230-0045, Japan
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l Similarity 15; Conser

Conservative

0

93.8%;

Score 15; Pred. No. Mismatches

DB 9; Le . 6.5e+03; ches 0;

Length 380;

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509959 MARC 3BOV Bos taurus
BM106270
sequence.
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15; Conserv
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Plate: 103 row: 0 column: 12
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, U: Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett Gasas,E., Wray,J.E., Legreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Cet
Bovidae; Bovinae; Bos.
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EST.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
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                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetlongissimus muscle."

94 c 102 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled"
/lab_host="DH10B"
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                               425 bp mRNA linear EST 08-MAR-2000 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2499846 3' contains TAR1.tl TAR1 repetitive element;, mRNA
                                                                                                                                                                                                                                                                93.8%; Score 15; DB 10; 100.0%; Pred. No. 6.5e+03;
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Insert Length: 822 Std Error: 0.00
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EST.
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AQ880479.1 GI:6311946
GSS.
                                                                                                                                                                                    AQ880479 507 bp DNA linear GSS 09-NOV-
HS_5044_A2_G02_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=8812 Col=4 Row=M, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                l Similarity
15; Conserv
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Seq primer: -40UP from Gibco
High quality sequence stp: 416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 425)
NCI/WINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                             Mahairas,G.G., Wallace
Keller,A., Shaker,R.,
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.
Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                             numan
                                                         (bases 1 to 507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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/clone_lib="NCI_CGAP_Brn25"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                    344
                                                                                                                                                                                                                                                                                                                                                                             93.8%;
                           Wallace,J.C., Smith,K., Swartzell,S., ker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
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ches 0;
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Adams,M.D. and
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Search completed: July 29, 2002, 23:22:40 Job time: 6816 sec
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                   scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

By 9380589

Contact; Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3618

Fax: (206) 616-387

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: B812 row: M column: 4

Seq primer: SP6

Class. BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 507.
Location/Qualifiers
1. .507
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141 a 117 c 107 g 135 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=8812 Col=4 Row=M"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                           93.8%; Score 15; DB
100.0%; Pred. No. 6.1
tive 0; Mismatches
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6.5e+03;
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Title: Perfect score: Sequence:

US-09-530-663B-15 16 1 cctttcaccaacccc

ccttcaccaacccc

Scoring table:

Gapop 10.0 , Gapext 1.0

IDENTITY_NUC

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nucleic search, using sw model

GenCore version Copyright (c) 1993 - 2000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-333-729A-2
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                                                                                                                                                                                   TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 16

SEQUENCE CHARACTERISTICS:

LENGTH: 1100 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

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                                                                                  Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/792498
ETLING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SVODOda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P104
TELECOMMUNICATION: 1NFORMATION:
TELEPHONE: 650/225-1489
mpt pray. 660/052-2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yang Wang
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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ON: O-Fucosyltransferase
CES: 17
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US-09-106-582-40
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Issued_Patents_Na:*

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2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

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6: /cgn2_6/ptodata/2,

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB Maximum DB

seq

length:

2000000000

Total number Searched:

0;

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NUMBER OF SEQ ID NOS: 2
SEQ ID NO 16
LEGGH: 1100
TYPE: DNA
ORGANISM: Homo Sapien
US-09-333-729A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08978741 Patent No. 6100076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1-3ubstitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/333,729A CURRENT FILING DATE: 1999-06-15 PRIOR APPLICATION NUMBER: US 08/798,741 PRIOR FILING DATE: 1997-11-26
                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                               NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DC
SOFTWARE: WinPatin (Ger
CURRENT APPLICATION DATA:
                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 cctttcaccaacctcc 181
                                                                                                                                                                                                                    APPLICATION NUMBER: 08/792498 FILING DATE: 31
             STRANDEDNESS:
                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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TOPOLOGY:
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        Nucleic Acid
Nucleic Acid
DEDNESS: Single
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California
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1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Francisco
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93.8%;
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Pred. No. 5
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CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 6
LENGTH: 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08978741 Patent No. 6100076
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Patent No. 6270987
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-FUCOSyltransferase
FILE REFERENCE: P1041P1D1-Successible File Reference:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
            APPLICATION NUMBER: 08/7:
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-Fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 CCTTTCACCAACCTCC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 cctttcaccaacctcc 316
                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
                                                                                                                       APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-No. 6100076-1997
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                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                        STREET:
REGISTRATION NUMBER:
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Pred. No. 52
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Pred. No. 52;
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GENERAL INFORMATION:
APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-FUCOSyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEG ID NOS: 21
SEQ ID NO 2
SEG ID NO 2
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Best Local 9
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INFORMATION FOR SEQ ID NO:
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TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 1514
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                                                              COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                             APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-FUCOSYltransferase NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   NERAL INFORMATION: APPLICANT: Yang W
CURRENT APPLICATION DATA:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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mes 15; Conserv
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               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                               COUNTRY:
                                                                                                                                                STREET: 1 DNA Way
CITY: South San Francisco
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                                                                                                 94080
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Pred. No. 53;
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; NUMBER OF SEQ ID NOS: ; SEQ ID NO 8; LENGTH: 5009; TYPE: DNA; ORGANISM: Homo Sapien US-09-333-729A-8
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; Patent No. 6270987
; GENERAL INFORMATION:
                                                                                                                      Sequence 5, Application US/08978741 Patent No. 6100076
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5009 base pairs
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
                                                                                                     GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                       NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESSE: Genentecle
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                     APPLICANT: Yang Wang, Michael W. Spellman
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STREET:
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South San Francisco
           1 DNA Way
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                          Genentech, Inc
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Pred. No. 61;
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Pred. No. 61;
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COUNTRY:

California

94080

1.44 Mb floppy disk

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APPLICANT: Naces, Peter S.
APPLICANT: Affholter, Joseph A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Affholter, Joseph A.
APPLICANT: AFFAILANT: US 208-463,903
CURRENT APPLICATION NUMBER: US 207/935,695
EARLIER APPLICATION NUMBER: US 207/935,695
EARLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 78
LENGTH: 79
munn: Num
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                                                                                                                                      ; NAME/KEY: DRb-3AH5' primer; LOCATION: 1..79
US-08-463-903-78
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                                                                  Query Match
Best Local Similarity
                                                     Matches
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Best Local :
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE, DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 Inch, 1.44 Mb |
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 11284 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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ctttcaccajacccc 15
                                                  14;
                                              87.5%; Score 14; DB ilarity 100.0%; Pred. No. 61 Conservative 0; Mismatches
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26-No. 6100076-1997
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Pred. No. 66;
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US-08-463-903-79
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; NAME/KEY: DRb-3AH5' primer
; LOCATION: 1..79
; OTHER INFORMATION: :
US-07-935-695-78
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LENGTH: 79
TYPE: DNA
                                                                                                                                                                                                                                                                                 SOFTWARE: MS-Word for Windows, Ver. 7.0 SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7 Patent No.
                                                                         Query Match
Best Local Similarity
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Best Local Similarity
Matches 14; Conserv
                                                        Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Affolter, Joseph A.
APPLICANT: Kotite, Nicolas J.
APPLICANT: Soseph A.
APPLICANT: Soseph A.
APPLICANT: Soseph A.
APPLICANTON UMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION UMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 78,
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Kotite, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms
FILE REFERENCE: 40224A US
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mezes, Peter S. APPLICANT: Richard, Ruth # APPLICANT: Affholter, Jose
                                                                                                                                                                                                     LENGTH: 95
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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2 ctttcaccaacccc 15
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o. 6071515
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                                                        Conservative
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                                                                     87.5%; Score 14;
100.0%; Pred. No.
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31 ctttcaccaacccc 44

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Query Match
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US-07-935-695-79
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US-08-485-657A-4
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SEQ ID NO 79
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Patent No. 6329507
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mezes, Peter S. APPLICANT: Richard, Ruth A APPLICANT: Affholter, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kotite, Nicolas J. TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides FILE REFERENCE: 40224A US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: DRb-3AHV3' primer LOCATION: 1..95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,657A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 95
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kirschling, De
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor
                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Genes and Genetic Elements Associated
TITLE OF INVENTION: with Sensitivity to Cisplatin
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                 NAME: NO. 5942389nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-N
                                                                                                            FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
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Affholter, Joseph A.
                                                                                                                                                                                                                                                                                                    USA
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100.0%;
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Pred. No.
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Search completed: July 29, Job time: 4754 sec
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Matches 14
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APPLICATION NUMBER: PC
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GENTITLE OF INVENTION: with NUMBER OF SEQUENCES: 25 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 206 base pairs
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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129 CATTTCACCAACCCC 143
                                                                         130 CATTTCACCAACCCC
                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TOPOLOGY: lin
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93.3%;
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93.3%;
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Pred. No. 1.4e+02;
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Pred. No. 1.4e+02;
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Sequence:

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
        Score
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length: 2000000000
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       Description
                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
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124588
LOCUS
DEFINITION
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VERSION
KEYWORDS
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Batter-Lowe,L.Ann.
Method for HLA Typing
Patent: US 5545526-A 16 13-AUG-1996;
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Sequence 16 from patent US
124588 124588.1 GI:1604458
                                                                                 Unclassified.
                                                                                       Unknown
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                                                 Location/Qualifiers
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AF093411
HSDRB13EX
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S57440S05
AU025871
S79786
AX237100
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HUMMHDR414
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HSDNAHLAB
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AR157073
AX128308
AX044055
AX044109
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AR097013
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AY022841
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AX128308 Sequence
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AX044059 Sequence
AX044109 Sequence
AX044059 Sequence
AX04505 Sequence
AR097013 Sequence
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AR097019 Sequence
AR097019 Sequence
AR09781 Homo sapi
AR034255 Sequence
AF406781 Homo sapi
AR04794 Human MHC c
M37771 Human MHC c
M37770 Human MHC c
M37770 Human MHC c
X55442 Human MHC c
X75347 H.sapiens D
X70788 H.sapiens H
AX022844 Homo sapi
AF028589 Homo sapi
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AF152845 Homo sapi
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AF093411 Homo sapi
X93315 H.sapiens H
L21985 Human major
L26306 Human DNA s
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127905 Sequence 7
127996 Sequence 2
127996 Sequence 2
128051 Sequence 2
128019 Sequence 9
A42460 Sequence 9
AR157073 Sequence
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PAT 07-OCT-1996

human STS

Database :

Maximum Minimum

DB DB

Result No.

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RESULT
I28051/c
LOCUS
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127905/c
LOCUS
DEFINITION
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VERSION
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ORIGIN
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AUTHORS
TITLE
JOURNAL
FEATURES
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SOURCE
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Apple,R.J., Erlich,H.A., Griff
Methods and reagents for HLA D
Patent: US 5567809-A 168 22-OC
Location/Qualifiers
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Apple,R.J., Erlich,H.A., Griffith,R.L. and Schamethods and reagents for HLA DRbeta DNA typing Patent: US 5567809-A 77 22-OCT-1996;
Location/Qualifiers
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      1 (bases 1 to 24)
Whittaker,J.L. and Morten,J.E.
HUMAN MHC CLASS II DOUBLE TRANSGENE AN
PAtent: WO 9503331-A 9 02-FEB-1995;
ZENECA LTD (GB)
Other publication AU 7231494 950220
Other publication GB 2280186 950125.
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Sequence 9 from Patent WO9503331.
A42460
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1 (bases 1 to 19)

Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J. Methods and reagents for HLA DRDeta DNA typing Patent: US 5567809-A 191 22-OCT-1996;
Location/Qualifiers
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Sequence 191 from patent
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Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.
Methods and reagents for HLA DRbeta DNA typing
Patent: US 5567809-A 223 22-OCT-1996;
Location/Qualifiers
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Sequence 10 from patent US
AR157073
AR157073.1 GI:15125777
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1 (bases 1 to 27)
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Sequence 9 from Patent W00066747.
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AX044109.1 GI:11342987
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1 (bases 1 to 39)
Hawkes,T.R., Warner,S.A., Andrews,C.J.,
Pickerill,A.P.
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Sequence 9 from Patent WO0066748.
AX044055 AX044055.1 GI:11342933
                                                                                                                                                                                                 Herbicide resistant plants Patent: WO 0066747-A 9 09-NOV-2000; ZENECA LIMITED (GB)
                                                                                                                                                                                                                                          artificial sequence.

1 (bases 1 to 39)

Hawkes,T.R., Warner,S.A., Andrews,C.J.,
Pickerill,A.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herbicide resistant plants
Patent: WO 0066748-A 9 09-NOV-2000;
ZENECA LIMITED (GB)
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/db_xref="taxon:32630"
/note="primer"
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/db_xref="taxon:32630"
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                          Score 11; DB 6;
Pred. No. 4.6e+04;
Mismatches 0;
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AR097013
AR097013.1
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Sequence 1354 from patent
AR040506
AR040506.1 GI:5959869
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Patent: WO 0066746-A 9 09-NOV-2000;
ZENECA LIMITED (GB)
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Hawkes,T.R., Warner,S.A., Andrews,C.J., Bachoo,S. and Pickerill,A.P.
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Sequence 9 from Patent W00066746.
AX044157
  Unknown
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Stinchcomb,D.T. and McSwiggen,J.A.
Interleukin-2 receptor gamma-chain ribozymes
Patent: US 5807743-A 1354 15-SEP-1998;
                                                                                                                                                                                                                                                                                                    Unknown.
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/db_xref="taxon:32630"
/note="Primer"
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32 TCTCACCAACC 42
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                                                                                    Oryza sativa microsatellite marker.

E15304
E15304.1 GI:5709987
JP 1998057073-A/28.
Oryza sativa
Dukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaa.

1 (bases 1 to 131)
Akagi, H., Fuiimura
Akagi,H., Fujimira,T., Yokozeki,S. and Inagaki,
MICROSATTELITE MARKER FOR DISCRIMINATING RICE P.
TEST FOR PURITY OF PLANT SEED
Patent: JP 1998057073-A 28 03-MAR-1998;
MITSUI PETROCHEM IND LTD
OS OTYZA SALIVA
PN JP 1998057073-A/28
PD 03-MAR-1998
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Sequence
AR097014
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Mezes, P.S., Richard, R.A., Affholter, J.A.
Dimer and multimer forms of single chain
Patent: US 6071515-A 77 06-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 69)
Mezes, P.S., Richard, R.A., Affholter, J.A.
Dimer and multimer forms of single chain
Patent: US 6071515-A 76 06-JUN-2000;
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25 c 17 g
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16 c 24 g
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41 TCTCACCAACC 31
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PR 13-JUN-1996 JP 96P 152657
PR AKAGI HIROMORI, FUJIMURA TATSUTO, YOKOZEKI SUKEYOSHI, PI INAGAKI AKIKO
PC CI2N15/09,C1201/68;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH SOURCE 1. 131
FT repeat_region 1. 131
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/organism='Oryza sativa'

Location/Qualifiers

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/organism="Oryza sativa"

/db_xref="taxon:4530"

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:/SIDS1/gcgdata/geneseq/geneseqn-emb1/Na1997.bAT: *
:/SIDS1/gcgdata/geneseq/geneseqn-emb1/Na1997.bAT: *
:/SIDS1/gcgdata/geneseq/geneseqn-emb1/Na1999.bAT: *
:/SIDS1/gcgdata/geneseq/geneseqn-emb1/Na1999.bAT: *
:/SIDS1/gcgdata/geneseq/geneseqn-emb1/Na1999.bAT: *
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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\SIDS1/gcgdata/geneseq/geneseqn-embl/NA2011A.DAT:*
\SIDS1/gcgdata/geneseq/geneseqn-embl/NA2011B.DAT:*
\SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

O	C	ဂ	ဂ	C	o	ဂ		a	No	Result
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match Length DB	Query
17	17	16	16	16	12	12	12	12	Length	
24	13	24	13	<u>1</u> 3	22	19	17	17	80	
ABL30817	AAQ26251	ABL31303	AAQ26196	AAQ26124	AAF92638	AAV16578	AAT41819	AAX79382	ID	
Human HLA genotypi	HLA-DR beta sub-ty	Human HLA genotypi	HLA-DR beta sub-ty	HLA-DR beta sub-ty	HLA-DR typing prob	Probe G86 used to	HLA allele, HLA-DR	HLA-DR typing prob	Description	

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ABL30757 ABL30757 ABC30750 AAQ06439 AAQ26219 AAQ79408 AAV794664 AAF92664 AAF9266594 AAQ9456594 AAQ9456594 AAQ9456594 AAC85374 AAC85374 AAC85374 AAC85374 AAC857155 AAC18184 AAC857155 AAC18184 AAC857155 AAC18184 AAC857155 AAC916156 AAF926156 AAF926156 AAF926157 AAC926156 AAF926157 AAC926156 AAF926157 AAC926156 AAF926157 AAC926156 AAF926157 AAC9261656 AAF9261656 AAF9261656 AAF9261656 AAF9261656 AAF9261656 AAF9261656 AAF9261656	AAS01746
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Human Oligo HLA-D HLA-D Gene Oligo Gene Oligo Human Mousee Human Micro Prime Prime Prime Prime Prime Prime La-D Human	Glu
Human HLA Human HLA Oligonucle HLA-DR bet HLA-DR by Probe VALB HLA-DR typ Probe vALB HLA-DR typin Oligonucle Human test Mouse alph Rice EPSPS Primer G1. Canine IL. Canine IL. Canine IL. Human secr Human secr Human foet Human foet Human bone Probe #195 Human bone P	Glucanase
Human HLA genotypi Human HLA genotypi Oligonucleotide pr HLA-DR beta sub-ty HLA-DR beta sub-ty HLA-DR typing prob Probe VAL86 used t HLA-DR typing prob Probe typing por Oligonucleotide pr Human testis speci Human secreted pro Microsatellite mar HLA-DR beta allele Human bone marrow Probe #19586 used Human haematologic Spleen necrosis vi Eucaryotic gene ex HLA-DR beta allele HLA-DR beta allele Arabidopsis thalia DRI *1105 allele DRB1*1305 allele DRB1*1305 allele BURL +DR beta allele DRB1*1305 allele DRB1*1305 allele	
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ALIGNMENTS

major histocompatibility complex; bone marrow transplant; primer; amplification; polymerase chain reaction; probe; polymorphism; sequence-specific oligonucleotide probe hybridisation; ss. Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;

RESULT 1
AAX79382;
ID AAX79382;
XX
AC AAX79382;
XX
DT 17-AUG-1999 (first entry)
XX
DE HLA-DR typing probe G86.
XX
Tissue typing; human leukocyte a major histocompatibility complex
KW major histocompatibility complex
KW amplification; polymerase chain
KW sequence-specific oligonucleotid
XX
PN US5468611-A.
XX
PN US5468611-A.
XX
PPD 21-NOV-1995.
XX
PPD 21-NOV-1995.
XX
PPF 08-APR-1993; 93US-0045530.
XX
PR 08-APR-1993; 93US-0045530.
XX
PA (BLOO-) BLOOD CENT RES FOUND INC
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PA (BLOO-) BLOOD CENT RES FOUND INC
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DR WPI; 1996-010091/01. (BLOO-) BLOOD CENT RES FOUND INC

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RESULT
AAT41819
ID AAT4
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Best Local S
Matches 11
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The sequences given in AAT41811-20 represent probes which were used to resolve the human leukocyte antigen (HLA) DRB1 atleles, DRB1*08, *12 and *1404. This probe sequence hybridises to the Gly86 coding region found in alleles *0801, *0802, *0803 and 0805. These probes may be used in the method of invention which concerns HLA typing of a sample for an unknown pair of alleles. The pair of alleles comprises one of two known types which have the same overall set of polymorphisms but have a different distribution of polymorphisms between their two alleles. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Improved method for HLA typing - by DNA amplification and sequence-specific oligo:nucleotide hybridisation, used to select bone marrow dohors
                                                                                                                                                                                  Human leukocyte antigen typing of tissue samples - using allele-specific amplification to distinguish allele pair
                                                                                                                                                                                                                                                                                                                                    01-MAR-1993;
27-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5545526-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human leukocyte antigen; HLA; allele; HLA-DR*08; HLA-DR*12; polymorphism; amplify; conserved region; detection; primer; tissue matching; identifying disease susceptibility; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA allele,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT41819 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A novel method of typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 19-20;
                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-1990;
                                                                                                                                                                                                                                                                                                    (BLOO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
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                                                                                                                                                  1; Column 19; 24pp; English.
                                                                                                                                                                                                                                                                                                    BLOOD CENT RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA-DRB1*08, *12 and *1404 resolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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90US-0544218.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
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Pred. No.
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                                                                                                                                                                                  distinguish allele pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17;
1.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probe,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  locus B1;
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Probes AAV16561-624 are used to identify differences in the DR region human major histocompatibility complex (HLA-DR). The specification describes a method for HLA-typing, which includes an oligonucleotide

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\begin{array}{c} \mathsf{CCCC} \\ \mathsf{CCC} \\ \mathsf{CCC} \\ \mathsf{XP} \\ \mathsf{X
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AAV16578/c
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HLA-DR beta
HLA-DR beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            method comprises selectively amplifying the DNA of just one allele of the unknown pair and analysing the amplified DNA to determine which polymorphisms are present in that allele, and therefore assigning the unknown pair to the known type having that allele. The method comprise three test stages. The first stage is to establish the number of alleles present in each sample. Primers corresponding to fairly well conserved regions of a locus will increase the likelihood that unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              may be done by amplification or hybridisation using a radiolabelled probe. The method may be used for tissue matching, identifying disease susceptibility, etc. The method of the invention esp. distinguishes between DQB1*0304/DQB1*03032 and DQB1*0301/DQB1*0302.
                                                                                                                                                                                                                                                    Oligo:nucleotide probes and primers and particularly for tissue typing for bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-1998
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                                                                                                                                                                Disclosure; Column 19; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baxter-Lowe LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BLOO-) BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUN-1990;
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Similarity 100.0%;
11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         major histocompatibility complex; HLA-DR; HLA-typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us sequence; allelic polymorphism;
polymorphism; probe; bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No.
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                                                                                                                                                                                                                                                                                            for HLA typing
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RESULT 4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe which undergoes sequence-specific hybridisation with an HLA-DR beta consensus sequence at positions 61-64. The probe contains a labelling substance other than a nucleotide sequence, which facilitates detection of the probe. The HLA sequence of a subject is PCR amplified, and a probe that recognises an allelic polymorphism at a selected HLA locus is contacted with the amplified product. This first probe recognises a HLA-DR beta-allelic polymorphism. A second (different) probe is brought into contact with a second sample of the amplified DNA in a separate reaction, and hybridisation detected. The probes and primers are used for HLA typing, e.g. for tissue, especially bone
                                                                                                  The present invention relates to human leukocyte antigen (HLA) typing The method involves detecting polymorphic residues by sequence specific oligonuclectide probe hybridization (SSOPH) with labeled
                                                                                                                                                                                   Human leukocyte antigen typing by amplifying a sample followed by sequence specific oligonucleotide hybridization with labeled oligonucleotide probes that hybridize with a series of known control DNA sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
SSOPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF92638 standard; DNA; 12 BP
                                                               Sequence
                                                                                                                                                                                                                                                                                                                           27-JUN-1990;
08-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-DR typing
                                                                                          oligonucleotide
                                                                                                                                                         Disclosure;
                                                                                                                                                                                DNA sequences
                                                                                                                                                                                                                                                                        Baxter-Lowe LA,
                                                                                                                                                                                                                                                                                                                                                                                                                    US6194147-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF92638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12 BP; 2 A; 0 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             marrow, transplants.
                                                                                                                                                                                                                                                                                                 (BLOO-) BLOOD CENT RES FOUND
                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 TCTCACCAACC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L
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                                                                                                                                                                                                                                                 2001-217923/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukocyte antigen; HLA; typing; sequence specific probe;
                                                                12
                                                                вP;
                                                                                                                                                     Column 11-14; 16pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe #18.
                                                                                                                                                                                                                                                                                                                         90US-0544218.
93US-0057957.
                                                                                                                                                                                                                                                                                                                                                                  97US-0000805
                                                                N
                                                                                        probes.
                                                                                                                                                                                                                                                                        Gorski JA;
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            100.0%;
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                                                                7
 0;
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                                                                                                                                                                                                                                                                                                   INC.
            Score 11; DB 22;
Pred. No. 1.9e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 11; DB 19;
Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 T; 0 other;
                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
 Mismatches
                                                               T; 0
                                                                other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,:
                        Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 12
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 Indels
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0;
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 Gaps
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0;
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RESULT 6
AAQ26196/c
ID AAQ261
XX
AC AAQ261
XX

AAQ26196

AAQ26196 standard; DNA;

16

ВP

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RESULT 5
AAQ26124/c
ID AAQ261
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 Вþ
                      Qy
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                                                           Query Match
Best Local (
                                                  Matches
                                                                                                                                    The sequence is that of the hybridising region of tailed probe DRB15 for use in a method for determining HLA-DR beta sub-type in a nucleic acid sample. The method allows specific nucleic acid sequences of the second exon of HLA-DR beta genes to be amplified then probed for identification of polymorphic sequences. The amplified DNA is useful for typing homozgous or heterozygous samples from a variety of sources and for detecting allelic variants not distinguishable by serological methods. The typing system can be used in a reverse dot blot format which is simple and rapid to perform, produces detectable signals in minutes and can be utilised in tissue typing, determination of individual identity and identifying disease susceptible individuals. Preliminary testing shows that the probe is more preferred than others. The probe is see also AAQ26092-Q26367.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Apple RJ,
Scharf SJ;
                                                                                                                                                                                                                                                                                                                                                        Method for determining HLA-DR beta sub-type in comprises amplification and hybridisation with primers, useful in tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ26124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ26124 standard; DNA; 16
                                                                                                               Sequence 16
                                                                                                                                                                                                                                                                                                                               Example; Page 37;
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-234644/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-DR beta sub-type tailed probe DRB15 hybridising region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JAN-1993
 13
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                       1 tctcaccaacc 11
TCTCACCAACC
                                                            Similarity
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                                                                                                               B₽;
                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identity determination; disease susceptible;
                                                                                                               2 A;
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                                                                                                                                                                                                                                                                                                                                90pp; English.
                                                           100.0%;
                                                                                                               2 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bugawan
                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΒP
                                                                                                               G;
                                                  0,
                                                            Score 11; DB 13;
Pred. No. 1.9e+03;
                                                                                                               4 T; 0 other;
                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
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                                                                          DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                               HΑ,
                                                                                                                                                                                                                                                                                                                                                                    probes
                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                       Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffith
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                  sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 RL;
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                                               Gaps
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RESULY 7
ABL31303/c
ID ABL313
XX ABL313
AC ABL313
XX 21-MAR
DT 21-MAR
XX Human;
KW Immunc
XX Immunc
XX Homo s
XX Homo s
XX PN WO2001
XX PPD 06-DEC
XX
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Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apple |
Scharf
              06-DEC-2001
                                                                                                                          Human HLA genotyping oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for determining HLA-DR beta sub-type in comprises amplification and hybridisation with primers, useful in tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue typing; identity determination; disease susceptible;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA-DR beta
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                                       WO200192572-A1
                                                               Homo sapiens.
                                                                                     Human; human leukocyte antigen; immunogenetic; transplantation;
                                                                                                                                                     21-MAR-2002
                                                                                                                                                                              ABL31303;
                                                                                                                                                                                                    ABL31303 standard;
                                                                                                                                                                                                                                                                                                                                                                             Sequence 16 BP; 2 A; 1 C; 9 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 39; 90pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-234644/28
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                                                                                                                                                                                                                                                                 TCTCACCAACC
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f SJ;
                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sub-type tailed
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                    (first entry)
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                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                            100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                             .0%;
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                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probe DRB92 hybridising region
                                                                                                                                                                                                                                                                                                                            Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                             4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG F.
                                                                                     HLA; genotype; polymorphism;
genetic disease; ss.
                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                             0 other;
                                                                                                                           SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erlich
                                                                                                                                                                                                                                                                                                                            DB 13;
1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HΑ,
                                                                                                                           NO 792
                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sample probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Griffith
                                                                                                                                                                                                                                                                                                                                        Length 16;
                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                0;
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RESULT 8
AAQ26251/c
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them, providing genetic information to decide compatibility of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucleotides (ABL30512-ABL31809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and
Method for determining HLA-DR beta sub-type in comprises amplification and hybridisation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organ and tissue for transplantation e.g. of bone marrow, kidney, liver, pancreas, Langerhans islet in pancreas and cornea, susceptibility diagnosis of genetic diseases and identifying individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human leukocyte antigen of individuals e.g. by d transplanting between th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                        Apple RJ,
Scharf SJ;
                                                                                                                                                                                                                         Tissue typing;
                                                                                                                                                                                                                                               HLA-DR beta sub-type tailed probe DRB147 hybridising region
                                                                                                                                                                                                                                                                       04-JAN-1993
                                                                                                                                                                                                                                                                                                                AAQ26251 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                   WPI; 1992-234644/28.
                                                                                         (HOFF ) HOFFMANN LA ROCHE & CO
                                                                                                               06-DEC-1990;
                                                                                                                                     06-DEC-1991;
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                                                                                                                                                                                WO9210589-A
                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                           AAQ26251;
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                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kagiya T,
                                                                   Begovich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                         identity determination; disease susceptible; ss
                                                                                                              90US-0623098
                                                                                                                                     91WO-US09294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 1 C;
                                                                                                                                                                                                                                                                                                                 DNA;
                                                                    AB,
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                                                                                                                                                                                                                                                                    entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                            .0%;
                                                                   Bugawan T,
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                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 T;
                                                                                         AG
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                          .
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsumura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ng, useful for immunogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                            No .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                    Erlich HA,
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 24;
1.9e+03;
DNA sample
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moriya
                                                                    Griffith RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           judging HLA
differences
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 16
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ß
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of the hybridising region of tailed probe DRB147 for use in a method for determining HLA-DR beta sub-type in a nucleic acid sample. The method allows specific nucleic acid sequences of the second exon of HLA-DR beta genes to be amplified then probed for identification of polymorphic sequences. The amplified DNA is useful for typing homozogous or heterozygous samples from a variety of sources and for detecting allelic variants not distinguishable by serological methods. The typing system can be used in a reverse dot blot format which is simple and rapid to perform, produces detectable signals in minutes and can be utilised in tissue typing, determination of individual identity and identifying disease susceptible individuals. It has not yet been tested. See also AAQ26092-Q26367.
                                                   The invention relates to a typing kit for judging human leukocyte an (HLA) genotype of a sample by hybridising a substrate on which 10-24 oligonucleotides (ABL30512-ABL31809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and
containing gene polymorphisms as alloantigens have been immobil primers for amplification of cleaved nucleic acids relating to polymorphisms. The method is useful for judging HLA genotypes c individuals by determining immunogenetic differences before tra
                                                                                                                         Claim 10; Page 151; 345pp;
                                                                                                                                                                    of individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL30817 standard; DNA; 17
                                                                                                                                                    transplanting between them
                                                                                                                                                                                 Human leukocyte antigen (HLA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genotyping
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Pred. No. 1.9e+03;
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Matches 11
                                 The sequence represents a sequencing primer for DNA encoding the Fusari fungal enzyme, glucanase. Glucanase, endochitinase and exochitinase are polypeptides with cell-wall degrading activity, derived from Fusari fungal genes. The associated nucleic acids can be used to produce transgenic plants which are resistant to plant pathogens, particularly Fusarium species. They can also be used to isolate homologous genes fro fungi to obtain genes which protect host cells, including fungi, bacter and plants against related fungal pathogens. The polypeptides, especial chitinases and glucanases, are useful for degrading seafood waste, such as shells that contain chitin, or for chemical modification of chitin o
                                                                                                                                                                                                                                                                                                                                                    (NOVO)
                                                                                                                                                                                                                                  Fusarium nucleic acids encoding polypeptides having glucanase, endochitinase or exochitinase activity, useful for producing transge plants which are resistant to plant pathogens, particularly Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-1999;
11-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between them, providing genetic information to decide compatibility organ and tissue for transplantation e.g. of bone marrow, kidney, lipancreas, Langerhans islet in pancreas and cornea, susceptibility diagnosis of genetic diseases and identifying individuals.
                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                          Okubara
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nilarity 100.
Conservative
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2000US-0224946.
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                                                                                                                                                                                                              The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucleotides (ABLJ0512-ABLJ1809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them, providing genetic information to decide compatibility of organ and tissue for transplantation e.g. of bone marrow, kidney, liver, pancreas, Langerhans islet in pancreas and cornea, susceptibility of diagnossis of genetic diseases and identifying individuals.
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                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen (HLA) typing, useful for of individuals e.g. by determining immunogenetic transplanting between them -
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Pred. No. 1.9e+03;
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differences
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transplanting between them
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                                                                    Oligonucleotide probe human type I diabetes
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                                 Insulin-dependent diabetes; systemic Reiter's disease; ss.
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genetic; transplantation;
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genetic disease; ss.
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe may be used in tests for proclivity towards autoimmune diseases such as insulin dependent diabetes, Reiter's disease Probes are highly specific, even able to differentiate between restriction fragments of identical size, and may also be used
                                                                             Method for determining HLA-DR beta sub-type in comprises amplification and hybridisation with primers, useful in tissue typing
                                                                                                                                                                           WPI; 1992-234644/28.
                                                                                                                                                                                                                      Apple RJ,
Scharf SJ;
                                                                                                                                                                                                                                                                                                                                 06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                        06-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue typing; identity determination; disease susceptible; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-DR beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQ beta gene oligo:nucleotide(s) - for detection of proclivity in humans for development of type I diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-341710/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1986;
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                                             Example;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ26219;
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                                           Page 40;
                                                                                                                                                                                                                                        Begovich
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illarity 100.0
Conservative
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                                      90pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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С;
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                                           English.
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                                                                                                                                                                                                                                        Bugawan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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                                                                                                                                                                                                                                           Erlich
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                                                                                                                                                                                                                                        HA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                      DNA sample probes and
                                                                                                                                                                                                                                        Griffith RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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the hybridising region

of tailed probe DRB115

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RESULT 15
AAX79408/C
ID AAX79408/C
ID AAX794
XX AAX794
XX T1SSUE
XX T1SSUE
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K
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue typing; human leukocyte antigen; HLA; MHC; donor; a major histocompatibility complex; bone marrow transplant; amplification; polymerase chain reaction; probe; polymorph sequence-specific oligonucleotide probe hybridisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for use in a method for determining HLA-DR beta sub-type in a nucleic acid sample. The method allows specific nucleic acid sequences of the second exon of HLA-DR beta genes to be amplified then probed for identification of polymorphic sequences. The amplified DNA is useful for typing homozgous or heterozygous samples from a variety of sources and for detecting allelic variants not distinguishable by serological methods. The typing system can be used in a reverse dot blot format which is simple and rapid to perform, produces detectable signals in minutes and can be utilised in tissue typing, determination of individual identity and identifying disease susceptible individuals.
                            A novel method of typing the human leukocyte antigen (HLA) of the major histocompatibility complex (MHC), esp. for typing donors for bone marrow transplants, involves determining if the donor tissue HLA-DR alleles are selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1, DR6a, DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c, B3, DR2a-d, B1, DR10 and DR1a-c. The method uses PCR to amplify these regions followed by sequence-specific oligonucleotide probe hybridisation (SSOPH) using the probes AAX79365-X79429. SSOPH allows detection of polymorphisms that predict differences at a single amino acid level thus reducing errors and improving the chance of successfully matching tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Improved method for HLA typing - by DNA amplification and sequence-specific oligo:nucleotide hybridisation, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-1990;
08-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                     Column 19-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                 donors
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93US-0045530.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorski JA;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  English.
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1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n; probe; polymorphism;
hybridisation; ss.
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AA052296 mb92902.r BE807681 ss29a0l.y BG342269 602374360 BI052985 RCO-GN027 BE033228 133585 MA

BE980472 UI-M-BG2-

AV028552 AV028552
AV028552 AV028552
AV028552 AV028552
AV0297032 RPCI-23-3
BG954331 CM4-CT065
AA061917 mj84a04.r
BE715956 MR2-HP075
BG133570 EST466558
AI137789 U1-R-E1-9
AV031373 AV031373
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BF07472 1c.99b01.y
AZ447050 1M0243b14
BM052472 1c.99b01.y
AZ447050 1M0243b10.r
BG195070 1M0243b10.r
BG195070 mm68bb10.r
BG195070 MR35670 AA576883 mR78410.s
BF645790 NF028F04E
AA718915 AH45411.s
AI705839 U1-R-AC1-AW836760 QV1-LT003
BE031039 129375 MA

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_est2:*
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AI292201
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 AA325418 EST28422
AA648082 ns10b07.r
BI040954 CM3-NT026
AZ753347 RPCI-24-1
AZ738998 RPCI-24-7
AI974770 T113239e
BI301600 UI-R-DLO-
BI562481 603256389
                                                                       AA184061 mo96f04.r
AA258662 zr61h08.r
BG953134 CM4-CT063
BF828693 MR2-HN003
BF085206 MR3-GN002
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AI292201 qm86e09.x
AZ233895 RPCI-23-8
                                                                                                                                                             Description
                                                                                                                                             AZ493433 1M0328A12
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ORGANISM
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AUTHORS
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VERSION
KEYWORDS
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AZ493433/c
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                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                           36 bp DNA linear GSS 05-OCT-2000 1M0328A12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0328A12 F, DNA sequence.
                                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                     High quality sequence stop:
Location/Qualifiers
                                                                                Plate: 0328 row: A column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
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AZ493433.1 GI:10667114
                                                                        Class: plasmid ends
                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                             nouse mouse
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="raxon:10090"
/clone="UUGC1M0328A12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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BF987685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Valle G.
CRIBI Biotechnology Centre
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                                                                                                                                                                                                                                                                                                                                                      ABI Chromatograms and other information are available on WWW at http://grup.bio.unipd.it.
                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Padua
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gblaF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                          /tissue_type="pectoral muscle (after mastectomy)", /note="Vector: pcDNAII (Invitrogen); Site_1: BstXI; Site_2: Not1: The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000090D07"
/clone_lib="HM3"
                                                The first strand cDNA was primed with a biotinylated
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/note="Vector:
                                                                                                                                                                               /sex="female"
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Pred. No. 1.6e+04;
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SOURCE KEYWORDS /ERSION POCUS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qm86e09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895656 3' similar to SW:TCPZ_HUMAN P40227 T-COMPLEX PROTEIN 1, ZETA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized Library was
                                                                                                                                                                                                                           /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                                                                                                                           constructed by Bento Soares and M. Fatima Bonaldo. 27\ c 19\ g 24\ t
                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1895656"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
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                                                                                                                                         TCTCACCAACC 73
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AA184061 108 bp mm mo96f04.rl Stratagene mouse testis (# clone IMAGE:567583 5', mmna sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC Library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Other_GSSs: RPCI-23-82M10.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Fraser, C.M.
Mouse BAC End Sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPCI-23-82M10.TV RPCI-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 102)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC ends.
                                                                                                                                                                                                                                                                                                                           /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRI Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-82M10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-23"
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                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                     Score 11;
Pred. No.
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Tsegaye,G., Geer,K., Krol,M.,
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                                                                                                                                                                                                                                                       DB 12;
                                         mRNA
                     (#937308) Mus musculus
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RPCI-23-82M10,
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                               AA258662.1
EST.
                                                                                                                                                                                                <code>zr61h08.r1</code> Soares_NhHMPu_S1 Homo sapiens cDNA clone 5', mRNA sequence. AA258662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu-
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
                                                                                                                                                                                                                                                      AA258662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA184061
AA184061.1 GI:1767429
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                            Homo sapiens
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                numan
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1 (bases 1 to 108)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="Inbred CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:567583"
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Pred. No.
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                                                                                          Euteleostomi;
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1 (bases 1 to 11)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Baria,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 bp mRNA lin
CM4-CT0639-220101-695-d02 CT0639 Homo sapiens
BG953134
                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                         sequence tags
                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                Simpson, A.J
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis,
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  +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                       Natl. Acad. Sci. U.S.A.
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/db_xref="taxon:9606"
/clone="IMAGE:667935"
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 120)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CT0639-
220101-695-d02&t3=2001-01-22&t4=1)
Seq_primer: puc 18 forward
                                                                                              This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2-MR2-HN0035-141200-015-e01&t3=2000-12-14&t4=1)
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BF828693
BF828693.1 GI:12173470
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Fax: +55-11-2707001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
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Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2-MR3-GN0029-110
900-004-f02_1&t3=2000-09-11&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 122)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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MR3-GN0029-110900-004-f02_1 GN0029
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                      /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse
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31 c 38 g 22 t 1 others
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/db_xref="taxon:9606"
/clone_lib="HN0035"
/dev_stage="Adult"
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/db_xref="taxon:9606"
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Pred. No.
of tissue mRNA and cDNA amplification were
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SOURCE

ORGANISM

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EST28422
AA325418
                                                                                                                                                                                                                                                                                                        For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter, J.C.
Initial assessment of human gene diversity and expression patterns
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bioinformatics
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                  /note="Organ: brain; Vector: pBluescript SK-;
ECORI; Site_2: XhoI"
34 c 44 g 26 t 3 others
                                                                                       /tissue_type="cerebellum"
/dev_stage="adult"
                                                                                                                                      /db_xref="ATCC (inhost):125942"
/db_xref="taxon:9606"
/clone_lib="Cerebellum II"
                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                  TCTCACCAACC 52
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ns10b07.rl
similar to
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     BI040954
BI040954.1
                                        sequence.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 124)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Seq primer: -28m13 rev1 ET from Amers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Cancer Institute, Cancer
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:966"
/clone="IMAGE:1183189"
/clone_lib="WCI_CGAP_Ew1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pAMP10; mRNA made from Ewing's sarcoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                                                                                                                                                                                                                             56:5380-5383.*
18 c '
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1 (bases 1 to 124)

Dias Neto,E., García Correa,R., Verjovskí-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baía,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeor
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                     Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                  , DNA sequence. AZ753347
                                                                                                                                                               GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human
Project. This entry can be seen in the following URL
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human.
                                                                      Mammalia; Eutheria;
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
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130201-748-d05_1&t5=2001-02-13&t4=1)
Seq primer: puc 18 forward-
High quality sequence stop: 119.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NT0268"
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Gebregeorgis,E.,
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; Murinae; Mus
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Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC
                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                             Unpublished (1999)
Other_GSSs: RPCI-24-71F6.TJ
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Other GSSs: RPCI-24-147P15.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
Department of Genomic Research
                                                              Email: szhao@tigr.org
                                                                                                                                                                                                                                Zhao,S., Nierman,W., Malek,J., Shatsman,S., A)
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 129)
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RPCI-24-71F6.TV
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC @
Page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 147 row: P column: 15
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301 838 0200
301 838 0208
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-147P15"
/clone=lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Cell_type="Spleen/Brain"
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_2: BamH1; Sites using MboI partially digested male C57BL/6J
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Plate: 71 row: F
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                       Other name: 02-KV2-3F4; date: 8/5/99; Submitted to the Database Expressed Sequence Tags (dbEST) on 08/25/99; More information is available at 'http://chrysie.tamu.edu/medicago'. Seq primer: SKmod (CTA gAA CTA gTg gAT CC).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
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T113239e KV2 Medicago truncatula
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VandenBosch, K., Hur
                                                                                                                                                                                                                                                                                                                      Email: kate@mail.bio.tamu.edu
                                                                                                                                                                                                                                                                                                                                                                                                   Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: VandenBosch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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ilarity 100.0%;
Conservative 0
                                                                               /cultivar="genotype Al
/db_xref="taxon:3880"
/clone="pKV2-1K8"
/clone_lib="KV2"
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                   /tissue_type="Seedling
/dev_stage="2 days post
meliloti"
                                                                                                                                                /organism="Medicago truncatula"
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/clone="RPCI-24-71F6"
/lab_host="E. coli strain SOLR"
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Search completed: July 29, 2002, 23:22:49 Job time: 6825 sec
                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                   Query Match 100.0%; Score 11; DB 9; Length 131; Best Local Similarity 100.0%; Pred. No. 2.2e+04; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                      1 teteaceaa¢c 11
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|112 TCTCACCAA¢C 102
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                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhOI; CDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells." a 13 c 43 g 53 t
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic search, using sw model
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length: 2000000000
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Match
          6:43:21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           July 29, 2002, 23:56:14 ; Search time 65.09 Seconds (without alignments) 41.511 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_NA: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
        US-08-025-038-16
US-08-050-073-17
US-08-050-073-191
US-08-050-073-191
US-08-050-073-191
US-08-050-073-191
US-08-463-903-76
US-08-463-903-77
US-07-935-695-77
US-08-039-137-16
US-08-039-137-16
US-08-025-038-33
US-08-025-038-33
US-08-025-038-33
US-08-025-038-33
US-08-025-038-33
US-08-025-038-33
US-08-050-073-1
US-08-050-073-1
US-08-050-073-13
US-08-050-073-13
US-08-050-073-13
US-08-050-073-15
US-08-050-073-15
US-08-050-073-15
US-08-050-073-15
US-08-050-073-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
Sequence 16, Appl Sequence 17, Appl Sequence 111, App Sequence 111, Appl Sequence 1154, Appl Sequence 1154, Appl Sequence 76, Appl Sequence 76, Appl Sequence 77, Appl Sequence 77, Appl Sequence 2, Appl Sequence 16, Appl Sequence 3, Appl Sequence 1, Appl Sequenc
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US-08-025-038-16
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                                                                                      Matches
                                                                                                       Query Match
Best Local Similarity
  1 totcaccaacc 11
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2 TCTCACCAACC 12
                                                                                  11;
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Result No.

Score

00000000

0 0 0 0 0 0 0 0 0 0 0 0 0 0

Conservative

0

Mismatches

0;

Gaps

0

100.0%;

Score 11; DB 1; Pred. No. 2.7e+02;

Length 12; Indels

Minimum Maximum

DB BG

seq

Scoring table: Sequence: Title: Perfect score:

Searched:

Run

OM nucleic -

Database :

ALIGNMENTS

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; LENGTH: 12 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single TOPOLOGY: linear US-08-025-038-16
                                                                                                                                                                                                                                                                                                CURRENT OF PARTICLE OF THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08025038 Patent No. 5545526 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 53202-5367

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BAXTER-LOWE, Lee-Ann
TITLE OF INVENTION: Method For HLA Typing
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 777 E. W
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
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RESULT 2 US-08-050-073-77/c

Application US/08050073

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APPLICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: US-08-050-073-77
                                                                                                                                                                                                                                    US-08-050-073-168/c
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 77, Appli
Patent No. 5567809
                                                                                                                                                                                                  Sequence 168, Application US/08050073 Patent No. 5567809
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                           APPLICANT: Apple, Raymond J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LATER APPLICANT Griffith, Robert L.
APPLICANT: Scharf, Stephen J.
TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
TITLE OF INVENTION: Typing
TITLE OF INVENTION: Typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: 1
APPLICANT: 1
APPLICANT: (
APPLICANT: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,07:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Methods
TITLE OF INVENTION: Typing
NUMBER OF SEQUENCES: 315
CORRESPONDENCE ADDRESS:
                                                                                                               APPLICANT: Begovich, Ann B.
APPLICANT: Bugawan, Teodorica L.
APPLICANT: Erlich, Henry A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                         13
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Jersey
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Bugawan, Teodorica L.
Erlich, Henry A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Hoffmann-La Roche Inc.
340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Griffith, Robert L.
Scharf, Stephen J.
VENTION: Methods and Reagents for HLA DRBeta DNA
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic DNA
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 11; DE 100.0%; Pred. No. 2.7 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/050,073
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                                                                                                                                                                                                                                                                                                                                                                                         DB 1; I
2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 16;
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US-08-050-073-223/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5567809
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 223, Application US/08050073 Patent No. 5567809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 16
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: I
APPLICANT: I
APPLICANT: I
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT: Griffith, Robert L.
APPLICANT: Griffith, Robert L.
APPLICANT: Scharf, Stephen J.
TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
TITLE OF INVENTION: Typing
TITLE OF SEOUENCES: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
COMPUTER: FOC POOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
ZIP: 07110
                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 340 K
                                                  FILING DATE:
                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                             CITY: Nutley
                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hoffmann-La Roche Inc. STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07110
                                                                                                                                                                                                           New Jersey
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                                                                                                                                                                                                                                                          E: Hoffmann-La Roche Inc.
340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                      Begovich, Ann B.
Bugawan, Teodorica L.
Erlich, Henry A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                      US/08/050,073
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Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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0

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-050-073-223
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                                                                      US-08-050-073-191
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEPEAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 191:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 191, Application US/08050073 Patent No. 5567809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (510) 814-2977 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Griffith, Robert L.
APPLICANT: Scharf, Stephen J.
TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
TITLE OF INVENTION: Typing
NUMBER OF SEQUENCES: 315
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Apple, Raymond J.
APPLICANT: Begovich, Ann B.
APPLICANT: Bugawan, Teodorica L.
APPLICANT: Erlich, Henry A.
APPLICANT: Griffith, Robert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                       STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Nutley
STATE: New Jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 TCTCACCAACC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8769
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tctcaccaacc 11
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                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 Kingsland Street
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                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoffmann-La Roche Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                       genomic DNA
                                                                                                                    single
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 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 11; DB 1;
Pred. No. 2.7e+02;
 Score 11; DB 1;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
                  Length 19;
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RESULT 7
US-08-758-306-1354/c
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; OTHER INFORMATION: Oligonucleotide ZC16,187
US-09-441-346A-10
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LENGTH: 25
TYPE: DNA
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PALENT NO. 580//...
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: MCSWiggen, James A.
APPLICANT: MCSWiggen, James A.
APPLICANT: MCSWIGGENT FOR /
APPLICANT NO DESCRIPTION: TREATMENT OF DISEASES
APPLICANT NO DESCRIPTION
APPLICANT NO DESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1354, Application US/08758306 Patent No. 5807743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O.
APPLICANT: Piddington, Christopher S
APPLICANT: Ellsworth, Jeff L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/109,216
PRIOR FILING DATE: 1998-11-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
PRIOR APPLICATION DATA:
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STREET: 633 West Fifth S
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          COMPUTER: IBM COMPONENTING SYSTEM: IBM P.C. OPERATING SYSTEM: IBM P.C. OPERATING SYSTEM FASTER OF THE PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                  APPLICATION NUMBER: FILING DATE: Decemb CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 TCTCACCAACC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 tctcaccaacc 11
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: FILING DATE:

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RESULT 9
US-07-935-695-76/c
                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
**-+-hes 11; Conserva
                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: 0101F primer
; LOCATION: 1..69
US-08-463-903-76
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TOPOLOGY:
US-08-758-306-1354
                                                                 GENERAL INFORMATION:
                                                                                   Sequence 76, Application US/07935695 Patent No. 6329507
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 76
LENGTH: 69
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 76, Application US/08463903 Patent No. 6071515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Affholter, Joseph A.
APPLICANT: Kotité, Nicolas J.
TITLE OF INVENTIÓN: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mezes, Peter S. APPLICANT: Richard, Ruth A.
                                 APPLICANT:
                                                   APPLICANT:
 APPLICANT:
                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
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11 TCTCACCAACC 1
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TELEX: 67-3510
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                Richard, Ruth A.
Affholter, Joseph A.
Kotite, Nicolas J.
                                                 Mezes, Peter S
                                                                                                                                                                                                                                                         100.0%; Score 11; DB 3; illarity 100.0%; Pred. No. 2.9e+02; Conservative 0; Mismatches 0;
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iilarity 100.0%;
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                                                                                                                                                                                                                                                                                         Length 69
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RESULT 11
US-07-935-695-77
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; LOCATION: 1..74
US-08-463-903-77
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Best Local Similarity
Watches 11; Conserve
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                                                                ; Sequence 77, Application US/07935695
; Patent No. 6329507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: MS-Word for Windows, Ver. 7.0 SEQ ID NO 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 77, Application US/08463903 Patent No. 6071515
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SEQ ID NO 76
APPLICANT:
APPLICANT:
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Best Local Similarity
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APPLICANT: KOLLLE, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms
FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides FILE REFERENCE: 40224A US CURRENT ENPLICATION NUMBER: US/07/935,695 CURRENT FILING DATE: 1992-08-21 PRIOR APPLICATION NUMBER: US 08/463,903 PRIOR FILING DATE: 1995-06-05 NUMBER OF SEQ ID NOS: 102 SOFTWARE: MS-Word for Windows, Ver. 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mezes, Peter S. APPLICANT: Richard, Ruth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: 0101F primer
LOCATION: 1..69
OTHER INFORMATION: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 69
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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Mezes, Peter S.
Richard, Ruth A.
Affholter, Joseph A.
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Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Single Chain Polypeptides
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APPLICANT:

Kotite, Nicolas

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RESULT 12
US-08-933-616-2
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US-08-933-616-2
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PENERAL INFORMATION:
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Best Local
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SOFTWARE: MS-Word for Windows, Ver. 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                            TELEFAX: (609) 466-2760 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: (
TITLE OF INVENTION: (
TITLE OF INVENTION: (
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: 0101R primer LOCATION: 1..74 OTHER INFORMATION: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 74
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                          REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD1-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/205,980 FILING DATE: 04-MAR 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Muccino
STREET: P.O. Box 1267
                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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Local Similarity 100.0%;
hes 11; Conservative
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32 tctcaccaacc 42
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STATE: New Jersey
                                                  STRANDEDNESS:
TOPOLOGY: unl
                                                                                                                                                                                                                                                                                                                                           FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/933,616
                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0855
                                                                   nucleic acid
EDNESS: unknown
                                                                                                                                                                                                                                               Muccino, Richard R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08933616
                                                                                                     220 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ON: Dimer and Multimer Forms of Single Chain Polypeptides
40224A US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Ralph C.
Cell-Type Specific Gene Transfer Using
Retroviral Vectors Containing Antibody-Envelope Fusion
Proteins and Wild-Type Envelope Fusion Proteins
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
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; LOCATION:
US-08-039-137-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16,
                                             Matches
                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TITLE OF INVENTION: Lent No. 5759771
                                                                                                                                                              HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 MOLECULE TYPE: cDNA to mRNA
247
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 350 Cam
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity nes 11; Conserv
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                                                         Local Similarity
                                                                                                                                                                                                                                                                                      TELEFAX:
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                     1 tctcaccaacc 11
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TCTCACCAACC
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                                                                                                                                                                                                                                   nucleic acid
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                                                                                                                                                                                                                                                268 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tilanus J.G., Marcel
VENTION: Method of Determining a Genotype by
VENTION: Comparing the Nucleotide Sequence of Members of a Gene
                                                                                                                                                                                                                                                                                       (415) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                            Conservative
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1..267
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                                                                                                                                                                                                                linear
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14-APR-1993
ON: 435
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237
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                                                       Score 11;
Pred. No.
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Pred. No. 3.2e+02;
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                                             Mismatches
                                                      3.2e+02;
                                                                     DB 1;
                                                                   Length 268;
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RESULT 14 US-08-025-038-32/c ; Sequence 32, Application US/08025038

Patent No. 5545526
GENERAL INFORMATION:

APPLICANT: BAXTER-LOWE, Lee-Ann TITLE OF INVENTION: Method For HLA Typing

46

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

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CURRENT APPLICATION NUMBER: US/08/025,000

APPLICATION NUMBER: US/08/025,000

FILING DATE: 1930301

CLASSIFICATION 435

PRIOR APPLICATION DATA: 45

APPLICATION NUMBER: 07/544,218

APPLICATION NUMBER: 1940

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Philip G.

REGISTRATION NUMBER: 30,478

REFERENCE/DOCKET NUMBER: 204 85/

TELECHONE: (414)289-3761

TELEPHONE: (414)289-3761

TELEFAX: (414)289-3791

TELEFAX: (414)289-3791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
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INFORMATION FOR $EQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                             Sequence 33, Application US/08025038
Patent No. 5545526
GENERAL INFORMATION:
APPLICANT: BAXTER-LOWE, Lee-Ann
TITLE OF INVENTION: Method For HLA Typing
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IHM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/025,038
FILING DATE: 19930301
CLASSIFICATION: 435
                                                                                                COUNTRY: USA
ZIP: 53202-5367
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 TCTCACCAACC 239
                                                                                                                                                                                                                   STATE: Wisconsin
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CITY: Milwaukee
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777 E. Wisconsin Avenue
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                                                                                Version #1.25
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Search completed: July 29, 2002, 23:56:14 Job time: 4755 sec
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                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative 0
                                                                                                                                                                                                                                                                                                                  TELEFAX: (414)289-3791 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Philip G.
REGISTRATION NUMBER: 30,478
REFERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 269 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 27-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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249 TCTCACCAACC 239
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Perfect score:
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Maximum Match 100%
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2: /SIDS1/gcgdata/g;
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A. DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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AAZ78756	AAZ77674	AAZ77645	AAZ50866	AAC81843	AAC81828	AAX23376	AAX59797	AAQ99824	ID
Human dendritic ce	Human dendritic ce	Human dendritic ce	Primer AP11 to ide	Gerbera flavone sy	Gerbera flavone sy	HLA-A, HLA-B, HLA-	Primer OPC6 for fu	Loblolly pine fusi	Description

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AAF42824 AAS99282 AAQ24014 AAQ65647 AAT13204	AAF41763 AAF41764 AAF41765 AAF41766 AAF42678	AAF38153 AAF39516 AAF39708 AAF40052 AAF40961 AAF41006	AAF35594 AAF36495 AAF36565	AAC91836 AAC93023 AAF33902 AAF34378 AAF35080 AAF35094	AAZ84187 AAZ85105 AAZ86191 AAH63480 AAH63759	AAZ79193 AAZ79337 AAZ81469 AAZ82818 AAZ83972
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ALIGNMENTS

RESULT 1 AAQ99824/c AAQ99824; AAQ99824 standard; cDNA; 10 BP

06-MAR-1996 (first entry)

Loblolly pine fusiform rust disease resistance marker OPC6 primer.

Lobbolly pine; Pinus taeda; fusiform rust disease; resistance marker; Cronartium quercum f.sp. fusiforme; Cqf; RAPD genetic marker; random amplified polymorphic DNA analysis; woody perennial plant; family selection; pedigree; mapping; primer; ss.

Synthetic.

W09519697-A1.

27-JUL-1995.

19-JAN-1995; 95WO-US00677

21-JAN-1994; 94US-0184567

(UYNC-) UNIV NORTH CAROLINA STATE.

WPI; 1995-269212/35.

Grattapaglia D, O'Malley DM,

Sederoff RR;

Determn. of heritable oligogenic traits in woody plants by genomic

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RESULT
AAX59797,
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Matches 6
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9797/c
AAX59797
                   associated with a genetic locus conferring resistance to fusiform rust disease in a family of trees of the genus Pinus. The method comprises obtaining a sexually mature Pinus parent tree exhibiting
  trees
                                                                                                 genus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cronartium quercuum f.sp. fusiforme (Cqf) the causative agent of fusiform rust disease, in lobbolly pine (Pinus taeda). A putative heterozygous mother tree (clone 10-5) and two open pollinated daughters (half-sib clones 152-231 and 152-257) were crossed to a highly susceptible pollen parent. Progeny were challenged with inoculum from various aeciospore lines. It was found that the marker amplified by the 10-mer primer in AAQ99824 was predictive resistance to inoculation with single Aeciospore line 2-36 in
                                                     The specification
                                                                           Example
                                                                                                                                 WPI; 1999-347038/29
                                                                                                                                                     Amerson HV,
Sederoff RR,
                                                                                                                                                                                                                                                                01-JUN-1999
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                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                         AAX59797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone 152-231 progeny. These and other results showed that resistance to fusiform rust disease in loblolly pine is under oligogenic control which can be mapped using genetic markers, using only a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mapping of multiple markers in a two generation plant family - to select plants with desired characteristics for breeding.
            resistance
                                                                                                         Identifying
                                                                                                                                                                                     (UYNC-) UNIV
                                                                                                                                                                                                          21-JAN-1994;
                                                                                                                                                                                                                    18-OCT-1995;
                                                                                                                                                                                                                                          18-OCT-1995;
                                                                                                                                                                                                                                                                                                                              tree family;
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                                                                                                           resistance
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                                                                                                                                                    Grattapaglia Wilcox P;
  parent
                                                                                                                                                                                     NORTH CAROLINA STATE
                                                                                                                                                                                                                                                                                                                               Pinus;
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                         95US-0545253
94US-0184567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pedigree
                                                                                                                                                                                                                                         95US-0545253
                                                                                                                                                                                                                                                                                                                              genetic locus; resistance;
nus; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                              fusiform rust disease resistance marker.
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                                                     describes a method of identifying
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                                                                                                          fusiform
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                                                                                                                                                                                                                                                                                                                                                                                                                             BP
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 disease, obtaining a p or cross-pollinations,
                                                                          English.
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1.1e+05;
                                                                                                          disease
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           a plurality
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                         probe
of ind
                                 allele containing the target polymorphisms, (b) labelling the single-stranded nucleic acid molecules, immobilising oligonucleotide probes, each specific for a known polymorphism, on a support and (c) detecting fully complementary duplexes formed between the labelled single-stranded nucleic acid molecules and the immobilised probes. The method is used for determining differences and correspondences in polymorphisms between individuals, tissues or organs by comparing hybridisation patterns produced by the above method. The method uses probe arrays rather than requiring sequential hybridisation and removal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    previous step. The method is userur row userum the previous step. The method is userur row in conting trees of the of resistance to fusiform rust disease and for producing trees of the pinus genus that are resistant to the disease. The present primer was pinus genus that are resistant or identify and amplify resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       progeny trees for a number of genetic markers, identifying genetic markers segregating in a Mendelian ratio and showing linkage with other genetic markers, measuring resistance to fusiform rust disease in multiple progeny trees and correlating the presence of resistance to fusiform rust disease with at least one marker identified in the previous step. The method is useful for determining the genetic basis
                                                                                                                                                   HLA-C allele by detecting polymorphisms using the primers AAX23371-X23380. The method involves (a) preparing single-stranc nucleic acid molecules corresponding in sequence to the portion
                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer; polymorphism; HLA-A; HLA-B; HLA-C; detection; probe array; hybridisation pattern; ss.
                                                                                                                                                                                                                                               polymorphism-specific
                                                                                                                                                                                                                                                           Hybridisation assay for identifying alleles
                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                Lee
                                                                                                                                                                                                                                                                                                                                       (LEES/)
                                                                                                                                                                                                                                                                                                                                                                 07-AUG-1997;
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                                                                                                                                    flavones that are useful as pharmaceuticals, e.g. in cancer treatment, as biologically active substances, e.g. to improve the immune defence system. Oligonucleotice fragments of (I) are used as probes and primers
                                                                                                                                                                     This invention describes a novel nucleic acid (I) that encodes flavone synthase II (FNSII) which has anticancer and immunomodulatory activity. FNSII catalyses conversion of naringenin to apigenin (I) is used to produce transgenic ornamental plants that have targeted alterations in flower color, also altered content/distribution of flavones in leaves, flowers and other tissues, e.g. increased resistance properties or symbbotic capacity. FNSII expressed by (I) is used in synthesis of
                                                                                                      Sequence
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                                                                                                                                                                                                                                                                 Example 4; Page 22; 40pp;
                                                                                                                                                                                                                                                                                                 New nucleic acid encoding flavone synthase II, useful e.g. for producing transgenic plants with altered flower color or flavone
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(FORK/) FORKMANN (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
         Tobacco plant; salicylic acid inducible gene; SA-inducible gene; transgenic plant; pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerbera; transgenic plant; flavone synthase II; FNSII; anticancer; immunomodulator; naringenin; apigenin; ornamental plant; flower colour; pharmaceutical; cancer; treatment; ss.
                                               Primer AP11 to
                                                                       31-MAY-2000
                                                                                               AAZ50866;
                                                                                                                       AAZ50866 standard;
                                                                                                                                                                                                                                                                                               Sequence 10
                                                                                                                                                                                                                                                                                                                                  as biologically active substances, e.g. to improve the immune desystem. Oligonucleotide fragments of (I) are used as probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding flavone synthase II, useful e.g. for producing transgenic plants with altered flower color or flavone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel nucleic acid (I) that encodes flavone
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                                                                     (first
                                              identify tobacco salicylic acid inducible genes
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1.1e+05;
hes 0;
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                      fungal pathogen;
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          primer;
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19-JUN-1998;
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AAZ77645 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses fifteen new salicylic acid (SA) inducible genes from Nicotiana tabacum, nine of which were subcloned and sequenced. Based on different kinetics of induction response, these genes were classified into four categories, class I, II, III and IV response genes. The SA-inducible genes are useful for making transgenic plants with enhanced pathogen resistance. The plants incorporating these genes show reduced susceptibility to fungal pathogens. The present sequence is an upstream primer API1 used in differential display PCR reactions along with downstream primers T12MG or T12MC to identify tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel salicylic acid inducible genes from tobacco plants, useful making transgenic plants with enhanced pathogenic resistance -
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                                                                         18-JUN-1999,
                                                                                                                   WO9965924-A2
                                                                                                                                        Homo sapiens
                                                                                                                                                            cytotoxic
                                                                                                                                                                  SAGE tag; serial analysis of gene expression; antigen-presenting ce APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
                                                                                                                                                                                                              Human dendritic cell SAGE tag,
                                                                                                                                                                                                                                     10-APR-2000
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                                                                                                                                                         T-lymphocyte;
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preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses.
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19-JUN-1998;
19-JUN-1998;
                                                these genes can be used in active immunotherapy (or to stimulate production of a population of antigen specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to Tell-rich sites, secretion of Tell growth factors and secretion of chemokines for
                                                                                                                                                                                                             an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell
                                                                                                                                                                                                                                                               They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or
                                                                                                                                                                          differentially expressed genes, or of their encoded proteins, can be to identify cells as belonging to the monocyte lineage. Cells contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESTs (expressed sequence tags) which were previously unknown to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAZ77573-Z79709 represent SAGE (serial analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 65; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotides differentially expressed cells, useful in gene vaccines against cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberts
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                  Isolated polynucleotides differentially expressed in cells, useful in gene vaccines against cancer -
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(ROBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes. or of their constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (APC) -associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic Tlymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly registed the tumour cells of the same several potential uses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of appulation of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to Tell-rich sites, secretion of Tell growth factors and secretion of chemokines for recruitment of immune effector cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentially expressed in monocyte-derived dendritic cells compared
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                                                                                                                                                                                                                                        SAGE tag; serial analysis of gene expression; antigen presenting APC; monocyte-derived dendritic cell; differential gene expression immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer
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immunostimulatory cofactor proteins which are preferentially or codifferentially expressed in monocyte-derived dendritic cells compared (C with monocytes, Some of the transcripts correspond to known genes or CC ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while (APC)-associated costimulatory factors play an important role in the ccorrespond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the CC activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone (C insufficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. (C They may be used in vaccines to induce an immune response, particularly capainst a tumour antigen; to modulate the genotype of an APC; to screen (C argainst a tumour antigen; to modulate the genotype of an APC; to screen (C argainst a tumour antigen; to modulate the genotype of an APC; to screen (C diagnosis, projnosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell expression of these genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing them are used in gene therapy (or to stimulate (C antigen searchain) to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory factors ensures adequate antigen presentation of co-stimulatory signals, migration of chemokines for the gressentation of immune effector cells.
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SHANKARA S.
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RESULT 10
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ID AAZ79193;
XX
AC AAZ79193;
XX
XY
DT 10-APR-2000 (first entry)
CE Human dendritic cell SAGE tag;
XX
SAGE tag; serial analysis of
KW APC; monocyte-derived dendrit
KW immunostimulatory cofactor; (
KW Cytotoxic T-lymphocyte; tumox
CS Homo sapiens.
XX
PN WO9965924-A2.
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PD 23-DEC-1999.
XX
19-JUN-1998; 98US-0089833.
PR 19-JUN-1998; 98US-0089853.
PR 19-JUN-1998; 98US-0089991.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0089997.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090040.
PR 19-JUN-1998; 98US-0090041.
PR 19-JUN-1998; 98US-0090042.
PR 19-JUN-1998; 98US-0090043.
PR 19-JUN-1998; 98US-0090044.
PR 19-JUN-1998; 98US-0090044.
PR 19-JUN-1998; 98US-0090044.
PR 19-JUN-1998; 98US-0090045.
PR 19-JUN-1998; 98US-0090044.
PR 19-JUN-1998; 98US-0090047.
PR 19-JUN-1998; 98US-0090047.
PR 19-JUN-1998; 98US-0090077.

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1.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells.
                                                                                                                                                                                         SAGE tag; serial analysis of gene expression; antigen-presenting ce APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other transcripts correspond to novel genes. Antigen-presenting cell (APC) associated costimulatory factors play an important role in the
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                   18-JUN-1999;
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Claim 1; Page 115; 130pp; English.
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19-JUN-1
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insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient to activation of cytotoxic Tymphocytes (CTLs). Nucleic acid sequences identified using the SACE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of anotherapy (or to stimulate users). vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene expression) tags used to identify mENA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendrific cells compared with monocytes. Some of the transcripts correspond to known genes particularly containing can be used o acid

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C AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour rissue (i.e. are upregulated in metastatic breast tumour cells). CAAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, cells). These transcripts can be used for diagnosis, prognosis, compitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification creactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while contents from the transcripts are used to direct expression, in selected contents of the transcripts are used to direct expression, and it is selected contents of the transcripts are used to direct expression of antisense concepts apricularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also concept the transcripts are also concept to the transcripts are also concept the transcripts are also concept the transcripts are also concept.
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        AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are promoters from the transcripts are used to direct expression, in selected
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19-JUN-1998;
19-JUN-1998;
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                                                                                                                                                                    Claim 1;
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        AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downzegulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10 BP; 1 A; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adoptive
                                                                           Claim
                                                                                              prevention
                                                                                                                                                       Roberts
                                                                                                                                                                                                                                                                                             23-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                       antimetastatic;
                                                                                                                                                                                                                                                                                                                                                                                            Metastatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ84187 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             potentially useful
                                                                                                                                                                          (SHAN/)
                                                                                                                                                                                                                                                       19-JUN-1998;
                                                                                                                                                                                                                                                                          18-JUN-1999;
                                                                                                                                                                                                                                             .9-JUN-1998;
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2 ccgttc 7
                                                                                                       non-metastatic breast
                                                                                                                                     2000-106079/09
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                                                                                                                                                                         GENZYME C
ROBERTS B
SHANKARA
                                                                                                                                                      BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                      polynucleotides differentially metastatic breast cancer cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunotherapy.
                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                            breast
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                      Shankara
                                                                           150;
                                                                                              treatment of
                                                                                                                                                                                  CORP.
                                                                                                                                                                                                                          98US-0090039
98US-0090040
                                                                                                                                                                                                                                             98US-0089997
                                                                                                                                                                                                                                                      98US-0089853.
                                                                                                                                                                                                                                                                          99WO-US13647
                                                                                                                                                                                                                                                                                                                                                      vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                            tumour
                                                                          219pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for treatment of (metastatic) breast cancer,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                            downregulated transcript
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                                                                                                                                                                                                                                                                                                                                                       ss.
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                                                                                                      expressed between metastatic useful for diagnosis,
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                                                                                                                                                                                                                                                                                                                                                              therapy; anticancer;
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AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour

transcripts

be used

Page

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Search completed: July 30, 2002, 00:01:19 Job time: 4930 sec
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 6; DB 21; Length 10; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells; e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 other;
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2 ccgttc 7
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Minimum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB seq length: 0
DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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AZ316663
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        AL467041 T. brucei
AL199669 qi60a02.x
AL242576 IM0236K13
AL2621312 IM0454P19
AL372925 IM0125D04
AL819947 ZM0091E20
AL493847 T. brucei
                                                                                     AA911671 0149f08.s

AZ347845 1M0084L06

AZ811866 2M0078M08

AZ653869 1M0527D14

AZ316663 1M0034G22

AZ436588 1M0224H20

AZ446206 1M0242106

AZ625200 1M0541G07

AZ789936 2M0038L17

AL467041 T. brucei
                                                                                                                                                                                                                                    Description
    T. brucei
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ORGANISM
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AA911671/c
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                        source
                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 682 Std Error: 0.00
Seg primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA911671 19 bp mRNA linear EST 10 0149f08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1526823 3' similar to TR:Q18444 Q18444 COSMID C34D4.
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                               ;contains MSR1.b2 MSR1 repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      AA911671.1 GI:3051035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inote-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver
                                                                                      /clone="IMAGE:1526823"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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AZ780363
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AI118841
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BJ055330
AQ050771
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BF168323
AZ642287
TA121A02P
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TA116E03P
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AZ4869974 2M0074C18
AZ809974 2M0074C18
AL451746 T. brucei
AL7451746 T. brucei
AL7451746 T. brucei
AL7451755 sb53h08.y
AZ780363 2M0017II1
AZ830168 2M0109E13
AL463260 T. brucei
BG719541 602690991
BG719541 602699891
AL7463260 T. brucei
BG719541 b02689891
AL74159 vz84e05.r
AL736496 sb59d11.y
N94283 za26f01.r1
AL450909 T. brucei
BF16323 601774306
AZ642287 1M0505D16
AL463540 T. brucei
AL451365 T. brucei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ347845 21 bp DNA li
1M0084L06F Mouse 10kb plasmid UUGC1M library
clone UUGC1M0084L06 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@enetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0084 row: L column: 06
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                     /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0084L06"
                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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5.9e+05;
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KEYWORDS
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AZ811866/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0078 row: M column: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads plasmid inserts % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS
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AZ811866.1 GI:12980548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone UUGC2M0078M08 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ811866 22 bp DNA linear GSS 20-FEB-200
2M0078M08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 22)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s: plasmid ends
quality sequence stop:
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                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
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                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biomedical
                                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC2M0078M08"
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/strain="C57BL/6J"
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Pred. No.
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6e+05;
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from a derivative
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AZ653869/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0527 row: D column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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AZ653869.1 GI:11791015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1M0527D14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0527D14 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
1 (bases 1 to 23)
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801 585 7177
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                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, /note="Vector: PMP42nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Jac Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg.,
                        adaptored DNA was purified and size-selected
                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0527D14"
                                                                                                                                                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                /sex="Male"
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kb range using preparative agarose gel
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0034 row: G column: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. University of Utah University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant vellocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg.,
                                                                                                                                                              Laboratory Mouse DNA Resource
                                                                                                                                                                                 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034G22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                         /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact Robert B. Weiss
University of Utah Genome Center
University of Utah
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1M0224H2OF Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0224H2O F, DNA sequence.
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Insert Length: 10000 Std Error:
Plate: 0224 row: H column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 molymerase molymerase and T4 molymerase molymer
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/clone="UUGC1M0224H20"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                   Seg primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 24.
                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through (0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 was blunt end-repaired with T4 DNA polymerase.
                                                                                                           /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                        Laboratory Mouse DNA Resource
                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0242I06"
                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                             /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 24.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: C
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
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and Wright,D.,Weiss,R.
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,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
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                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, /note="Vector: PWD42nv; Purified genomic DNA from Nusculus C57BL/6J (male) was obtained from the Jac
                                                                                             Laboratory Mouse DNA Resource
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/clone="UUGC1M0541G07"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ789936 24 bp DNA linear GSS 16-FEB-200 2M0038L17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0038L17 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                       Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0038 row: L column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg.,
                                                                                           /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                       Laboratory Mouse DNA Resource
                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC2M0038L17"
                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                /sex="Male"
                                                                                                                                                                                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Pred. No.
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6.1e+05;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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SOURCE

VERSION

Locus

RESULT

BASE COUNT ORIGIN

RESULT 10 TA143H10Q

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Matches

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Query Match
Best Local
                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       nhisanger.ac.uk

nhisanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically shear

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically shear

to give a tight size distribution (

4 kD). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects.

Genome Sequencing: A Practical Approach, eds. M. Yaudin and B.

Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hicambridge CB10 15A, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 24)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Hall, N., Bowman, S., Cannard, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence.
AL467041
AL467041.1 GI:11836396
                                                                                                                                                                                                                                                                                                           Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                             Email: nelsayed@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Conservative
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                                                                                                                                          /organism="Trypanosoma k
/strain="TREU927"
/db_xref="taxon:5691"
/clone="143h10"
a 3 c 9 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            purified. The sheared, agaptored into adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."

a 10 c 5 g 5 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                        Score 6;
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Pred. No.
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BASE COUNT ORIGIN

Matches

dq

DNA

linear

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FEATURES

source

COMMENT

REFERENCE

AUTHORS

TITLE JOURNAL

SOURCE

ORGANISM

KEYWORDS VERSION

ACCESSION DEFINITION

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BASE COUNT
ORIGIN
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AI199669/c
                RESULT 12
AZ442576/c
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TITLE
                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                           Matches
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                                                                                                                       1 ccgttc 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trace considered overall poor quality Insert Length: 654 Std Error: 0.00 Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortlum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 25)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
AZ442576
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                         6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                      13
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                          /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1860842"
/clone_lib="NCI_CGAP_Brn25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                         100.0%;
                                                                                                                                                           0;
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Pred. No.
                                                                                                                                                           Mismatches
 25
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6.1e+05;
hes 0;
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 GSS 04-OCT-2000
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RESULT 13
AZ621312/c
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Insert Length: 10000 Std Error: (
Plate: 0236 row: K column: 13
Seq primer: CACACAGGAAACACTATGACC
Class: plasmid ends
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Fax: 801 585 7177
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1 (bases 1 to 25)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0236K13"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
Plate: 0454 row: P column: 11
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1M0454P19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0454P19 F, DNA sequence.
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Contact: Robert B.
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                                                                                                       Conservative
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/note="Vector: PW042nv; Purified genomic DNA from M.
musculus CS7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="UUGC1M0454P19"
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/strain="C57BL/6J"
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Insert Length: 10000 Std Error:
Plate: 0125 row: D column: 04
Seg primer: CGTTGTAAAACGACGGCCAGT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
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Fax: 801 585 7177
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                                                                                                         Conservative
                                                                                                                                                                                                                     http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNASMIGHT of properties of pNASMIGHT. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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/db_xref="taxon:10090"
/clone="UUGC1M0125D04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
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100.0%; 5
tive 0;
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Pred. No. 6.2
0; Mismatches
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6.2e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. We
University of Utah Ge
University of Utah
Rm. 308, Biomedical E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 bp DNA linear GSS 20-FEB-201
2M0091E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0091E20 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 0091 row: E column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ819947.1 GI:12989855
GSS.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0091 row: E column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 26)
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                                                                                                                                                                                  /note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114/gb1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                    adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for amplcillin resistance."

9 c 4 g 10 t
                                                                                                                              with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC2M0091E20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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6 Similarity

Conservative

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Mismatches

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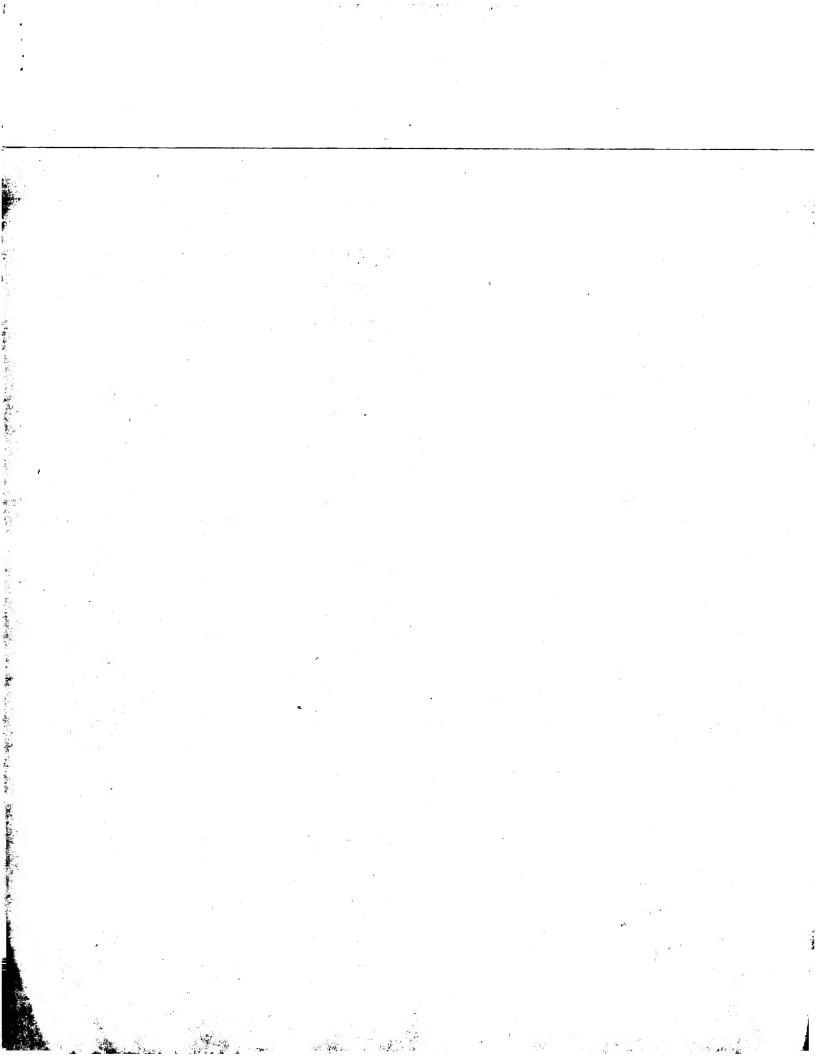
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Score 6; Pred. No.

DB 12; I . 6.2e+05; .ches 0;

Length 26; Indels

Search completed: July 29, 2002, 23:22:44 Job time: 6820 sec



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Maximum Match 100%
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Perfect score:
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       Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/
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3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
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6: /cgn2_6/ptodata/2/
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length: 2000000000
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-853-028-6
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US-08-15-061-10
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US-08-95-162-1835
US-08-95-162-1835
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US-08-9774-306A-26
US-08-9774-306A-27
US-09-064-156A-27
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                             Sequence 2, Appli Sequence 8, Appli Sequence 8, Appli Sequence 10, Appli Sequence 10, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 8, Appli Sequence 8, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 21, Appli Sequence 27, Appli Seq
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Mismatches

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Gaps

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Score 6; Pred. No.

DB 2; L 2.5e+07; 0, Length 9; O

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43,	Sequence 43, Appl	Sequence 43, Appl	Sequence 521, App	Sequence 3, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 15, Appl	Sequence 14, Appl	Patent No. 5182195	Sequence 14, Appl	Sequence 26, Appl	Sequence 17, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 11, Appl	Sequence 14, Appl	Sequence 4, Appli

ALIGNMENTS

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; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA
US-08-642-045B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08642045B Patent No. 5851804 GENERAL INFORMATION:
                                                                                                                                              TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION UNMBER: 33,229
REFERENCE/DOCKET NUMBER: APOL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
TELEPAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: WINDOWS
SOFTWARE: WORDERFECT 6.0/6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Snyder, Linda A.
APPLICANT: Satishchandran, C.
APPLICANT: Satishchandran, C.
TITLE OF INVENTION: CHIMERIC KANAMYCIN RESISTANCE GENE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5851804ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 06-MAN CLASSIFICATION: 51
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US-08-852-268-4/c
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                                                                                                                                                                         Sequence 8, Application US/08545253A Patent No. 5908978
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APPLICANT: Pachuk
                                                                                                                                                       GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CHAIN REACTION CLONING NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOORDOO'S
STREET
                                                                          APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Une CITY: Philadelphia STATE: Pennsylvania
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-MAY-1996
CLASSIFICATION: 435
             TITLE OF INVENTION:
                                             TITLE OF INVENTION:
                                                                                                         APPLICANT: O'Malley, David M. APPLICANT: Sederoff, Ronald R APPLICANT: Grattapaglia, Dari
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DeLuda, Mark
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                                                                                                Local Similarity
les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION | NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                     8 CCGTTC 3
                                                                                                                                                                                                                                                                                               1 ccgttc 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 base pairs
                                                                                                         Grattapaglia, Dario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pachuk,
                             E, George Kuhlman
VENTION: METHODS FOR WITHIN FAMILY
VENTION: SELECTION IN
                                                                          Henry V. Amerson
Phillip Wilcox
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           both
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100.0%; F
ative 0;
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WOODY PERENNIALS USING GENETIC MARKERS 26
                                                                                                                      Ronald R.
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Pred. No. 2.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                             DB 3; Le 2.5e+07;
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Query Match
Best Local Similarity
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US-08-719-337-8/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-08-545-253A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08719337 Patent No. 6054634
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: O'MAlley, David M.

APPLICANT: Sederoff, Ronald R.

APPLICANT: Grattapaglia, Dario

TITLE OF INVENTION: METHODS FOR WITHIN FAMILY SELECTION IN

TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: SLbley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-281
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               CLASSIFICATION: 047 PRIOR APPLICATION DATA:
                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
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                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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CITY: Charlotte
CTATE: No. 5908978th Carolina
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                  STREET: Post Off
APPLICATION NUMBER: 08/1 FILING DATE: 21-JAN-1994
                                                                   APPLICATION NUMBER: FILING DATE: 25-SE
                                                                                                                                                                                                                   COUNTRY: UZIP: 28234
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                                                                     25-SEP-1996
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                                                                                      US/08/719,337
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ATTORNEY/AGENT INFORMATION:

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RESULT 6
US-07-974-447-10
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Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                                    Matches
                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO 0605
FILING DATE: 21 June 1996
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (919) 881-31
TELEX: 575102
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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ADDRESSEE: D. Peter Hochberg Co., L.P.A.
STREET: The Baker Building - Sixth Floor 1940 East 6th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                       TYPE: Nucleic Acid
STRANDEDNESS: Doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,665 REFERENCE/DOCKET NUMBER: 50
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/878,835A FILING DATE: June 19, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
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                                                                                                                    Conservative
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                                                                                                                                                                                                          Linear
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Pred. No.
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Pred. No.
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RESULT 7
US-08-149-199-10
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Best Local Similarity
...+ches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/07974447 Patent No. 5436142 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08149199 Patent No. 5501964
                                                                                                                                                                                                                        Patent No. 3002200
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H
APPLICANT: Lisitsyn, Nikolai
APPLICANT: Lisitsyn, Nikolai
ARBPRESENTATIONAL APPROACH TO GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 781-1
TELEFAX: (415) 398-324
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORIEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-57
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PCDOS/MSDOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
COPPRESSION OF THE PC-DOS/MS-DOS
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APPLICATION NUMBER: US/0:
FILING DATE: 12-NOV-1992
                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
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APPLICANT: Lisitsyn, Nikolai
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ZIP: 941
                                                                                              COUNTRY:
ZIP: 941
                                                                                                                               CITY: San Francisco
STATE: California
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STATE: California
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4 Embarcadero Center,
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                                                                                                                USA
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100.0%; Pred. No.
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                                                                                                                                                                      TEST, ALBRITTON & HERBERT er, Suite 3400
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149
FILING DATE: 9-No. 5501964-93

US/08/149,199

ATTORNEY/AGENT INFORMATION:

FILING DATE: 9-CLASSIFICATION:

0;

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US-08-411-727-5/c; Sequence 5, Application US/08411727; Patent No. 5705161; Patent No. 5705161 5683703
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TELEX: 910 277299
INFORMATION FOR $FQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative C
                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: NL 9201716
FILING DATE: 02 OCT-1992
PRIOR APPLICATION NUMBER: WO PCT/NL93/00163
APPLICATION NUMBER: WO PCT/NL93/00163
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATÍON:
APPLICANT: VAN DEI
APPLICANT: POOLMAI
APPLICANT: HOOGERI
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 3225
REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: I pm PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A57438/BIR CSHL002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 7811989
TELEFAX: (415) 3983249
TELEX: 910 2777000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: IMMUNOGENIC MENINGOCOCCAL LPS AND OTHER TITLE OF INVENTION: MEMBRANE VESICLES AND VACCINE THEREFROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/411,727
FILING DATE: 01-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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Y: U.S.A.
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POOLMAN, Jan Theunis
HOOGERHOUT, Peter
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Query Match Best Local Similarity

100.0%;

Score 6; Pred. No.

1.6e+04; DB

Length 12;

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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-411-727-5
; MOLECULE TYPE: US-08-411-727-6
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Patent No. 5705161
Patent No. 5705161 5683703
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Matches 6; Conserv
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                                                                                                                       TELEX: 248425 EMBON INFORMATION FOR SEQ ID NO:
                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
                                                                                                                                                                                                         FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 329;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: NL 9201716
FILING DATE: 02-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/NL93/00163
FILING DATE: 30-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VAN DER LEY, Peter Andre
APPLICANT: POOLMAN, Jan Theunis
APPLICANT: HOOGERHOUT, Peter
TITLE OF INVENTION: IMMUNOGENIC MENINGOCOCCAL LPS AND OTHER
TITLE OF INVENTION: MEMBRANE VESICLES AND VACCINE THEREFROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/411,727 FILING DATE: 01-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                  TOPOLOGY:
                                                 STRANDEDNESS:
                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virginia
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     745 South 23rd Street, Suite 200
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                DNA (genomic)
                                               single
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Pred. No.
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RESULT 11
US-08-858-767-8
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                                 GENERAL INFORMATION:
APPLICANT: WANG, X.
APPLICANT: DUVICK,
APPLICANT: BRIGGS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                     Sequence 8, Application US/08858767 Patent No. 5837468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5837468
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 33229/325/PIHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 19-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
APPLICANT: DUVICK, Jonathan P. APPLICANT: BRIGGS, Steven P. TITLE OF INVENTION: PCR-BASED TITLE OF INVENTION: METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/481,687 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DUVICK, Jonathan P.
APPLICANT: BRIGGS, Steven P.
TITLE OF INVENTION: PCR-BASED (
TITLE OF INVENTION: METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3000 K STREET: Washington
                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                       h 100.0%;
Similarity 100.0%;
6; Conservative 0;
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                                                                    WANG, Xun
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                                                                                                                                                                                                                                                                                                                                                                            linear
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                   PCR-BASED CDNA SUBTRACTIVE CLONING
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Mismatches
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hes 0;
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                                                                                                                                                                                                                                                                                                      Length 12;
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                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: 19-Max-1997
CLASSIFICATION: 43-5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,028
                                                                                                                                                                                                                                                  TITLE OF INVENTION: PC:
TITLE OF INVENTION: ME'
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 333
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                      APPLICANT: DUVICK, Jonathan P. APPLICANT: BRIGGS, Steven P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WANG, Xun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 100.0%; Score 6; DB Local Similarity 100.0%; Pred. No. 1.0 hes 6; Conservative 0; Mismatches
                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                    STREET: 3000 K S CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BENT, Stephen A REGISTRATION NUMBER: 2
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 CLASSIFICATION:
                                                                                                                                                                                                                                       ADDRESSEE:
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3000 K Street, N.W., Suite 500
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3000 K Street, N.W., Suite 500
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SYSTEM: PC-DOS/MS-DOS
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19-MAY-1997
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                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION (NUMBER: US/08/858,767
FILING DATE: 19-MAY-1997
APPLICATION NUMBER: US 08/481,687
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
               INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
                                                                        REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
STATE: D.C.
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APPLICANT: DTVICK, Jonathan P.
APPLICANT: BRIGGS, Steven P.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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nes 6; Conserv
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TYPE: nucleic acid
STRANDEDNESS: single
                                 TELEX:
                                             TELEFAX:
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20007-5109
CHARACTERISTICS:
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                                               : (202)672-5300
(202)672-5399
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Pred. No.
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APPLICANT: Migler, Michael
APPLICANT: Lisitsyn, Nikolai
TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO DNA ANALYSIS
FILE REFERENCE: CSHL.002.04US
CURRENT APPLICATION NUMBER: US/09/261,079
CURRENT FILING DATE: 1999-03-02
EARLIER APPLICATION NUMBER: 08/478,242
EARLIER APPLICATION NUMBER: 08/478,242
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-01-07
EARLIER APPLICATION NUMBER: 07/974,447
EARLIER FILING DATE: 1995-01-07
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 12
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Best Local Similarity
"hes 6; Conserv:
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; STRANDEDNESS: sing
; TOPOLOGY: linear
US-08-863-028-8
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US-09-261-079-10
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SEQ ID NO 10
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 08/149,199
EARLIER FILING DATE: 1993-11-09
EARLIER APPLICATION NUMBER: 07/974,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1998-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wigler, Michael APPLICANT: Lisitsyn, Nikolai TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO DNA ANALYSIS FILE REFERENCE: CSHL.002.03US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1992-11-12
NUMBER OF SEQ ID NOS: 20
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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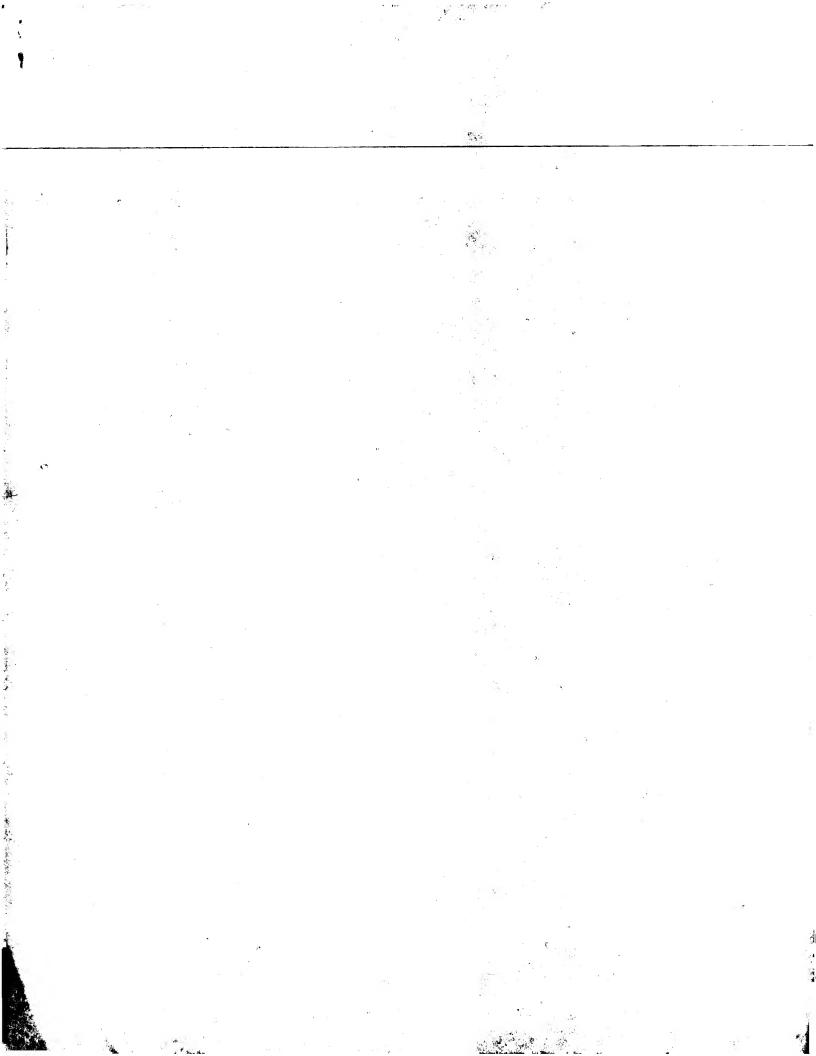
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: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: DESCRIPTION of Artificial Sequence:
: OTHER INFORMATION: OLIGONUCLEOTIDE
US-09-261-079-10

Query Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: July 29, 2002, 23:56:14

Job time: 4755 sec
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AR070974 Sequence AX043779 Sequence AX152405 Sequence AX152684 Sequence AX301586 Sequence

A38146 Sequence

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Title:
Perfect score:
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Description
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                 JOURNAL
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                                              1 (bases 1 to 10)
Amerson,H.V., Wilcox,P., Sederoff,R.R., O'Malley,D.M. and Grattapaglia,D.
Methods for within family selection of perennials using genetic markers
Patent: US 5908978-A 801-UN-1999;
                                                                                                          Unknown
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Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
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Martens,S. and Forkmann,G.
Genetic sequence which codes for the
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Patent: WO 0065073-A 11 02-NOV-2000;
Martens, Stefan (DE); Forkmann, Ger
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Patent: WO 0138577-A 320 31-MAY-2001;
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Patent: WO 0138577-A 599 31-MAY-2001;
The Johns Hopkins University (US)
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                                                                                                                                                                                                                                             Wang, X., Duvick, J.P. and Briggs, S.P. PCR-based CDNA substractive cloning Patent: US 5837468-A 6 17-NOV-1998; Location/Qualifiers
                                                                                                                                                                                                                                                                                         Unclassified.
1 (bases 1 to 12)
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Van,D.L., Poolman,J.T. and Hoogerhout,P.
IMMUNOGENIC MENINGOCOCCAL LPS AND OUTER MEMBRANE VESICLES
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/db_xref="taxon:32644"
/clone="PJBOO7"
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Sequence
AR068444
                                   1 (bases 1 to 12)
Wang, X., Duvick, J.P. and Briggs, S.P.
PCR-based cDNA subtractive cloning m
Patent: US 5853991-A 8 29-DEC-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   Wang,X., Duvick,J.P. and Briggs,S.P.
PCR-based cDNA subtractive cloning method
Patent: US 5853991-A 6 29-DEC-1998;
Location/Qualifiers
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Sequence 6 from
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Wang, X., Duvick, J.P. and Briggs, S.P.
PCR-based cDNA substractive cloning
Patent: US 5837468 A 8 17-NOV-1998;
Location/Qualifiers
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Wigler, M. and Lisitsyn, N.
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Wigler, M. and Lisitsyn, N.
Methods for producing pro
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Patent: US 6159713-A 10 12-DEC-2000;
Cocation/Qualifiers
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US 5436142-A 10 25-JUL-1995;
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AUTHORS
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BD000935
LOCUS
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FEATURES
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Best Local Similarity
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Britania K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.C.

Holesek, J.J. and Mamone, A.J.

Method and reagent for inhibiting viral replication

Patent: JP 2000342285 A 95 12-DEC-2000;

RIBOZYME PHARMACEUTICALS INC

Artificial Sequence

PN JP 2000342285-A/95

PD 12-DEC-2000

PF 01-MAY-2000 JP 2000132616

PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/88271

14-MAY-1992 US 07/88283,14-MAY-1992 US 07/88281

14-MAY-1992 US 07/88283,14-MAY-1992 US 07/88282

14-MAY-1992 US 07/88283,14-MAY-1992 US 07/88282

14-MAY-1992 US 07/88288,14-MAY-1992 US 07/88282

14-MAY-1992 US 07/88289,14-MAY-1992 US 07/88292

14-MAY-1992 US 07/88289,14-MAY-1992 US 07/88493

14-MAY-1992 US 07/88292,14-MAY-1992 US 07/88433

14-MAY-1992 US 07/884422,14-MAY-1992 US 07/88433

14-MAY-1992 US 07/884422,14-MAY-1992 US 07/88443

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14-MAY-1992 US 07/884422,14-MAY-1992 US 07/88433

14-MAY-1992 US 07/98338,26-NUG-1992 US 07/88433

14-MAY-1992 US 07/98332,07-DEC-1992 US 07/987133

15-CCT-1992 US 07/98332,07-DEC-1992 US 07/987133

07-DEC-1992 US 07/987330,07-DEC-1992 US 07/987133
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JP 2000342285-A/95.
 PI JAN
PC C11
C12N15,
PC C11
CCC
FH Key
FT SOU
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119029
119029.1
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related sources
Patent: US 5501964-A 10 26-MAR-1996;
Location/Qualifiers
1. .12 "...brown"
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Wigler, M. and Lisitsyn, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      artificial sequence.

1 (bases 1 to 14)
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                                                                                                                                                       MAYSEJAK,
                                                                                                                                                                        KENNETH G DRAPER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methods
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                                                                                                           JAMES J HOLESEK, ANTHONY J MAMONE C12N15/09, C12N5/10, C12N7/00, C12N9/22//(C12N5/10, C12R1:91),
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                     source
                                       Key
                                                                            C12N5/00, (C12N5/00, C12R1:91)
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10 from patent US 5501964.
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3 c 3 g
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192 US 07/882689,14-MAY-1992 US 07/882713,14-MAY-1992 US 07/88

107/882713,14-MAY-1992 US 07/88

107/882886,14-MAY-1992 US 07/88

107/882889,14-MAY-1992 US 07/88

107/882889,14-MAY-1992 US 07/88

107/882922,14-MAY-1992 US 07/88

107/883849,14-MAY-1992 US 07/88

107/884474,14-MAY-1992 US 07/88

107/884472,14-MAY-1992 US 07/88

107/884436,14-MAY-1992 US 07/88

107/984382,14-MAY-1992 US 07/88

107/983322,07-DEC-1992 US 07/93

107/963322,07-DEC-1992 US 07/98

107/987130,07-DEC-1992 US 07/98

107/987130,07-DEC-1992 US 07/98

107/987130,07-DEC-1992 US 07/98

107/987130,07-DEC-1992 US 07/98
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                                     Location/Qualifiers
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Pred. No. 1.6
0; Mismatches
/organism='Artificial Sequence'
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07/88224 PR
07/882284 PR
07/882288 PR
07/882291 PR
07/88323 PR
07/884073 PR
07/884331 PR
07/884331 PR
07/884331 PR
07/884521 PR
07/884521 PR
07/98723 PR
07/987129 PR
07/987139 PI
1GEN, PI DENNIS G
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RESULT 15
BD001364
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BASE COUNT
ORIGIN
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AUTHORS
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ORIGIN
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Best Local Similarity
Matches 6; Conserv
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OS Artificial Sequence
PN JP 2000342286 - A/95
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132651
PF 11-MAY-1992 US 07/88283,14-M
14-MAY-1992 US 07/88289,14-M
14-MAY-1992 US 07/883849,14-M
14-MAY-1992 US 07/883842,14-M
14-MAY-1992 US 07/884422,14-M
14-MAY-1992 US 07/884422,14-M
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14-MAY-1992 US 07/88436,14-M
14-MAY-1992 US 07/88436,14-M
14-MAY-1992 US 07/88436,14-M
31-UL-1992 US 07/936086,26-A
31-UL-1992 US 07/936322,07-D
07-DEC-1992 US 07/963322,07-D
                                                                                                                                                        C12R1:93)
CC
FH Key
FT Source
                                                                                                                                                                                                                                                                                                                   MAYSEJAK,
PI JAME
PC C12N
PC A61K
PC A61K
PC A61P
PC A61P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Draper, K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.G., Holsesk, J.J. and Mamone, A.J. Method and reagent for inhibiting viral replication Patent: JP 2000342286-A. 95 12-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD001364.1 GI:18625923
JP 2000342286-A/95.
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1 (bases 1 to 14)
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                                                                                                                                                                                                                                                                                  A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC (C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
                                                                                                                                                                                                                                                                                                                                                              A61K39/135,
A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
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                                                                                                                                                                                                                                                                                                                                                                                                                   JAMES J HOLESEK, ANTHONY J MAMONE
C12N15/09/C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
                                                                                                                                                                                    source
              /organism='Artificial Location/Qualifiers
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/db_xref="taxon:32630"
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1. .14
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07/882714
07/88284
07/882868
07/882868
07/88231
07/88433 p
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07/88433 p
07/88433 p
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07/98729 pi
07/987129 pi
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Search completed: July 29, 2002, 23:55:06 Job time: 7022 sec